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TECH CENTER 1600 2000

- 1 -

SEQUENCE LISTING

<110> Lowery E., David
Fuller E., Troy
Kennedy J., Michael

<120> Anti-Bacterial Vaccine Compositions

<130> 28341/6227.1

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<150> 60/153,453
<151> 1999-09-10

<150> 60/128,689
<151> 1999-04-09

<160> 165 ,

<170> PatentIn Ver. 2.0

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aacaatagtt ttaaacaata ttottccatt ttttataagt aagtacttaa atataaagca 180
tttcataaaa tatcaataaa ggatttagtt atg gca gca gag ctt aca aca gcg 233
Met Ala Ala Glu Leu Thr Thr Ala
1 5

gga tat att ggg cac cat tta gca ttc ttg aaa aca ggg gat tct ttc 281
Gly Tyr Ile Gly His His Leu Ala Phe Leu Lys Thr Gly Asp Ser Phe
10 15 20

tgg cat gtt cat tta gat acc ctt cta ttt tca att att tca ggt gca 329
Trp His Val His Leu Asp Thr Leu Leu Phe Ser Ile Ile Ser Gly Ala
25 30 35 40

att ttt ctt ttt gtt ttt tca aaa gtt gca aaa aaa gca acg ccg ggt 377
Ile Phe Leu Phe Val Phe Ser Lys Val Ala Lys Lys Ala Thr Pro Gly
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Val Pro Ser Lys Met Gln Cys Phe Val Glu Ile Met Val Asp Trp Ile	
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Asp Gly Ile Val Lys Glu Asn Phe His Gly Pro Arg His Ala Val Gly	
75 80 85	
cca tta gca tta act att ttc tgc tgg gta ttc att atg aat gct atc	521
Pro Leu Ala Leu Thr Ile Phe Cys Trp Val Phe Ile Met Asn Ala Ile	
90 95 100	
gat ttg atc cca gta gat ttc cta cct caa tta gcc cat tta ttt ggt	569
Asp Leu Ile Pro Val Asp Phe Leu Pro Gln Leu Ala His Leu Phe Gly	
105 110 115 120	
att gaa tac tta aga gct gtt cca aca gca gat atc agt gga aca tta	617
Ile Glu Tyr Leu Arg Ala Val Pro Thr Ala Asp Ile Ser Gly Thr Leu	
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ggc tta tca att ggt gtc ttc ttc tta att att ttc tat aca atc aaa	665
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140 145 150	
tca aaa ggt atg agt ggc ttt gtt aaa gaa tat acg ctt cat cct ttt	713
Ser Lys Gly Met Ser Gly Phe Val Lys Glu Tyr Thr Leu His Pro Phe	
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Leu Leu Ala Lys Pro Val Ser Leu Ala Phe Arg Leu Phe Gly Asn Met	
185 190 195 200	
tat gca ggt gaa ctt atc ttt att ctt att gca gtg atg tac atg gca	857
Tyr Ala Gly Glu Leu Ile Phe Ile Leu Ile Ala Val Met Tyr Met Ala	
205 210 215	
aat aat ttt gca ctt aat tca atg ggt att ttc atg cat ttg gct tgg	905
Asn Asn Phe Ala Leu Asn Ser Met Gly Ile Phe Met His Leu Ala Trp	
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Ala Ile Phe His Ile Leu Val Ile Thr Leu Gln Ala Phe Ile Phe Met	
235 240 245	
atg ctt aca gtg gtt tat ttg agt atg ggt tat aac aaa gca gaa cac	1001
Met Leu Thr Val Val Tyr Leu Ser Met Gly Tyr Asn Lys Ala Glu His	
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<213> Pasteurella multocida

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Val Ala Lys Lys Ala Thr Pro Gly Val Pro Ser Lys Met Gln Cys Phe
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Val Glu Ile Met Val Asp Trp Ile Asp Gly Ile Val Lys Glu Asn Phe
65 70 75 80

His Gly Pro Arg His Ala Val Gly Pro Leu Ala Leu Thr Ile Phe Cys
85 90 95

Trp Val Phe Ile Met Asn Ala Ile Asp Leu Ile Pro Val Asp Phe Leu
100 105 110

Pro Gln Leu Ala His Leu Phe Gly Ile Glu Tyr Leu Arg Ala Val Pro
115 120 125

Thr Ala Asp Ile Ser Gly Thr Leu Gly Leu Ser Ile Gly Val Phe Phe
130 135 140

Leu Ile Ile Phe Tyr Thr Ile Lys Ser Lys Gly Met Ser Gly Phe Val
145 150 155 160

Lys Glu Tyr Thr Leu His Pro Phe Asn His Pro Leu Leu Ile Pro Val
165 170 175

Asn Leu Ala Leu Glu Ser Val Thr Leu Leu Ala Lys Pro Val Ser Leu
180 185 190

Ala Phe Arg Leu Phe Gly Asn Met Tyr Ala Gly Glu Leu Ile Phe Ile
195 200 205

Leu Ile Ala Val Met Tyr Met Ala Asn Asn Phe Ala Leu Asn Ser Met
210 215 220

Gly Ile Phe Met His Leu Ala Trp Ala Ile Phe His Ile Leu Val Ile
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tatgcgtgag ttaacccaat ctggcaatta caatgatgaa attaaagagt cattaaaagg 300
cattttggat agcttcaaag caaacagtgc gtggtaagtt aacactttaa atggagagac 360
aaa atg gca ggt gct aaa gag ata aga acc aaa atc gcg agt gta aaa 408
Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys
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agt aca caa aaa att act aaa gcg atg gaa atg gtt gct gcc tcg aaa 456
Ser Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys
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Met Arg Lys Thr Gln Glu Arg Met Ser Ser Ser Arg Pro Tyr Ser Glu
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aca ata cgt aac gtg att agc cac gtt tcc aaa gca acg att ggt tac 552
Thr Ile Arg Asn Val Ile Ser His Val Ser Lys Ala Thr Ile Gly Tyr
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Lys His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile
65 70 75
gtt gtg tcc aca gat cgt ggt ctt tgt ggt ggc tta aac gtg aac ttg 648
Val Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Val Asn Leu
80 85 90 95
ttt aaa act gta tta aat gaa atg aaa gaa tgg aaa gaa aaa gat gtt 696
Phe Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val
100 105 110
tcc gtt caa ttg agt tta atc ggt tct aaa tct atc aac ttt ttc caa 744
Ser Val Gln Leu Ser Leu Ile Gly Ser Lys Ser Ile Asn Phe Phe Gln
115 120 125
tct ttg gga att aaa att tta acc caa gat tca ggt att ggt gat act 792
Ser Leu Gly Ile Lys Ile Leu Thr Gln Asp Ser Gly Ile Gly Asp Thr
130 135 140
ccc tct gtt gag cag tta att ggt tca gtc aat tct atg att gat gct 840
Pro Ser Val Glu Gln Leu Ile Gly Ser Val Asn Ser Met Ile Asp Ala
145 150 155
tat aaa aaa ggg gaa gta gat gtt gtg tat tta gtt tat aac aaa ttt 888
Tyr Lys Lys Gly Glu Val Asp Val Val Tyr Leu Val Tyr Asn Lys Phe
160 165 170 175
att aac acg atg tcg caa aag cca gta ttg gaa aaa tta att cca tta 936
Ile Asn Thr Met Ser Gln Lys Pro Val Leu Glu Lys Leu Ile Pro Leu
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Tyr Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val	
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cgt tat tta gaa tct cag gtt tat caa gca gca gtt gaa aac ctt gct	1080
Arg Tyr Leu Glu Ser Gln Val Tyr Gln Ala Ala Val Glu Asn Leu Ala	
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tct gag caa gcc gct cga atg gtc gcc atg aaa gca gca aca gat aac	1128
Ser Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn	
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Gln Ala Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala	
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35 40 45

Ile Arg Asn Val Ile Ser His Val Ser Lys Ala Thr Ile Gly Tyr Lys
50 55 60

His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile Val
65 70 75 80

Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Val Asn Leu Phe
85 90 95

Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val Ser
100 105 110

Val Gln Leu Ser Leu Ile Gly Ser Lys Ser Ile Asn Phe Phe Gln Ser
115 120 125

Leu Gly Ile Lys Ile Leu Thr Gln Asp Ser Gly Ile Gly Asp Thr Pro
130 135 140

Ser Val Glu Gln Leu Ile Gly Ser Val Asn Ser Met Ile Asp Ala Tyr
145 150 155 160

Lys Lys Gly Glu Val Asp Val Val Tyr Leu Val Tyr Asn Lys Phe Ile
165 170 175

Asn Thr Met Ser Gln Lys Pro Val Leu Glu Lys Leu Ile Pro Leu Pro
180 185 190

Glu Leu Asp Asn Asp Glu Leu Gly Glu Arg Lys Gln Val Trp Asp Tyr
195 200 205

Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val Arg
210 215 220

Tyr Leu Glu Ser Gln Val Tyr Gln Ala Ala Val Glu Asn Leu Ala Ser
225 230 235 240

Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala
245 250 255

Gly Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln
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Ala Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala
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Glu Phe Tyr Pro Leu Glu Ala Val Lys Thr Asn Ile Leu Gly Thr Ala
20 25 30
96

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Asn Val Leu Glu Ala Ala Ile Gln Asn Gln Ile Lys Arg Val Val Cys
35 40 45
144

ctt agc aca gat aaa gcg gtc tac cca att aat gcg atg ggc att tct
Leu Ser Thr Asp Lys Ala Val Tyr Pro Ile Asn Ala Met Gly Ile Ser
50 55 60
192

aaa gca atg atg gaa aaa gtc atc atc gca aaa tcg cgt aac cta gaa
Lys Ala Met Met Glu Lys Val Ile Ala Lys Ser Arg Asn Leu Glu
65 70 75 80
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Gly Thr Pro Thr Ile Cys Cys Thr Arg Tyr Gly Asn Val Met Ala
85 90 95
288

tcg cgt ggt tcg gtt atc cca tta ttt gtc gat caa ata cgt caa ggc
Ser Arg Gly Ser Val Ile Pro Leu Phe Val Asp Gln Ile Arg Gln Gly
100 105 110
336

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115 120 125
384

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432

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Asn Gly Asp Val Phe Val Gln Lys Ala Pro Ala Ala Thr Ile Gly Thr
145 150 155 160
480

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Leu Ala Lys Ala Ile Thr Glu Leu Leu Ser Val Pro Asn His Pro Ile
165 170 175
528

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Ser Ile Ile Gly Thr Arg His Gly Glu Lys Ala Phe Glu Ala Leu Leu
180 185 190
576

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Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg
195 200 205
624

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Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys
210 215 220
672

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Gly Glu Pro Lys Ile Thr Glu Val Thr Asp Tyr Asn Ser His Asn Thr
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720

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245 250 255	
ttc ata cag aaa atg att gag ggt gaa tac atc tca ccg gag gta	813
Phe Ile Gln Lys Met Ile Glu Gly Glu Tyr Ile Ser Pro Glu Val	
260 265 270	
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Leu Ala Lys Ala Ile Thr Glu Leu Leu Ser Val Pro Asn His Pro Ile
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Ser Ile Ile Gly Thr Arg His Gly Glu Lys Ala Phe Glu Ala Leu Leu
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Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg
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Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys
210 215 220
Gly Glu Pro Lys Ile Thr Glu Val Thr Asp Tyr Asn Ser His Asn Thr
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gag aaa att gca caa gaa ttg tta gcg tat agc tta gaa ggt cgc cct 4118
Glu Lys Ile Ala Gln Glu Leu Leu Ala Tyr Ser Leu Glu Gly Arg Pro
15 20 25
gtg cat att tcc tta tcc gga ggc tca acg ccg aaa ttg tta ttt aaa 4166
Val His Ile Ser Leu Ser Gly Ser Thr Pro Lys Leu Leu Phe Lys
30 35 40 45
act tta gct caa gca ccg tat aac acc gag att caa tgg aaa aat ttg 4214
Thr Leu Ala Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu
50 55 60
cat ttt tgg tgg ggc gat gat cgt atg gtg cca cca acc gat cca gaa 4262
His Phe Trp Trp Gly Asp Asp Arg Met Val Pro Pro Thr Asp Pro Glu
65 70 75

agt aat tac ggc gag gtg caa aaa ttg tta ttc gat cat att cag atc 4310
Ser Asn Tyr Gly Glu Val Gln Lys Leu Leu Phe Asp His Ile Gln Ile
80 85 90

cct gca gaa aat att cac cgc att cgt ggt gaa gcc ccc gtt gag agt 4358
Pro Ala Glu Asn Ile His Arg Ile Arg Gly Glu Ala Pro Val Glu Ser
95 100 105

gaa ctt cac cgt ttt gaa caa gcg cta agt gcg gtc att cct ggg caa 4406
Glu Leu His Arg Phe Glu Gln Ala Leu Ser Ala Val Ile Pro Gly Gln
110 115 120 125

gtt ttt gat tgg att att ttg ggc atg gga acg gac ggg cac acg gcc 4454
Val Phe Asp Trp Ile Ile Leu Gly Met Gly Thr Asp Gly His Thr Ala
130 135 140

tca tta ttc ccg cat caa acc gat ttt gac gat cct cat ttc gcc gtc 4502
Ser Leu Phe Pro His Gln Thr Asp Phe Asp Asp Pro His Phe Ala Val
145 150 155

atc gcg aaa cac cct gaa aca ggg caa att cgt att tca aaa aca gcg 4550
Ile Ala Lys His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala
160 165 170

aaa ttg att gaa caa gca aag cgg gtg acc tat ttg gtg aca ggt agc 4598
Lys Leu Ile Glu Gln Ala Lys Arg Val Thr Tyr Leu Val Thr Gly Ser
175 180 185

agt aaa gcc gag atc tta aaa gaa att caa act act ccg gca gaa caa 4646
Ser Lys Ala Glu Ile Leu Lys Glu Ile Gln Thr Thr Pro Ala Glu Gln
190 195 200 205

ctg cct tat cct gct gcg aaa atc aaa gcg aag cat ggg gtg acg gaa 4694
Leu Pro Tyr Pro Ala Ala Lys Ile Lys Ala Lys His Gly Val Thr Glu
210 215 220

tgg tat ttg gat aag gat gcg gca aaa tta ctg taatgcgtcg tgagatttt 4747
Trp Tyr Leu Asp Lys Asp Ala Ala Lys Leu Leu
225 230

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ctgaaaatga aggctctcggt tgaaaatggc gccatttgtt gggtaagctt aaggttcgct 4867

cagacagcgc tatcaaaagg gtaaaagaat gtatcaactc tattttaaatc cacaaaaatc 4927

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<211> 232
<212> PRT
<213> Pasteurella multocida

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35 40 45
Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu His Phe Trp
50 55 60
Trp Gly Asp Asp Arg Met Val Pro Pro Thr Asp Pro Glu Ser Asn Tyr
65 70 75 80
Gly Glu Val Gln Lys Leu Leu Phe Asp His Ile Gln Ile Pro Ala Glu
85 90 95
Asn Ile His Arg Ile Arg Gly Glu Ala Pro Val Glu Ser Glu Leu His
100 105 110
Arg Phe Glu Gln Ala Leu Ser Ala Val Ile Pro Gly Gln Val Phe Asp
115 120 125
Trp Ile Ile Leu Gly Met Gly Thr Asp Gly His Thr Ala Ser Leu Phe
130 135 140
Pro His Gln Thr Asp Phe Asp Asp Pro His Phe Ala Val Ile Ala Lys
145 150 155 160
His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala Lys Leu Ile
165 170 175

Glu Gln Ala Lys Arg Val Thr Tyr Leu Val Thr Gly Ser Ser Lys Ala
180 185 190

Glu Ile Leu Lys Glu Ile Gln Thr Thr Pro Ala Glu Gln Leu Pro Tyr
195 200 205

Pro Ala Ala Lys Ile Lys Ala Lys His Gly Val Thr Glu Trp Tyr Leu
210 215 220

Asp Lys Asp Ala Ala Lys Leu Leu
225 230

<210> 9
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<220>
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gaagctgcgc accctgatat cgaattatat accgcattcag ttgatagtca cttaaatgaa 180
caaggctata ttattccagg tcttgggtat gccgggtata aaattttgg cactaaataa 240
tcccaacaca agcggcatct tatgccgtt tttccgttc aatttatacg gcttacaatc 300
ttaacagctt gaacactata aaatgaaaag ttaattcaga cagagagttg aaacttaaca 360
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ttaagggtta agtc ttg ctt aac cct tca ttt ttc gtt tat cct tat tct 1670
Leu Leu Asn Pro Ser Phe Phe Val Tyr Pro Tyr Ser
1 5 10
cct ttt ttc gat ttt gta ggt tgc ttt ttg tta gaa aat ttc caa tta 1718
Pro Phe Asp Phe Val Gly Cys Phe Leu Leu Glu Asn Phe Gln Leu
15 20 25
cct ttg cct att cat caa ctc gat gat gaa acg ctg gat aat ttc tat 1766
Pro Leu Pro Ile His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr
30 35 40
ccc gac aat aat tta ttg ttg ctc aat tcg cta cgc aaa aat ttt act 1814
Pro Asp Asn Asn Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr
45 50 55 60
tgt cta aca caa caa ttt ttt tat att tgg ggc gag caa agc agt ggt 1862
Cys Leu Thr Gln Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly
65 70 75
aaa agt cac ctc tta aaa ggc att act cat cat ttt ttc ctt tta cag 1910
Lys Ser His Leu Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln
80 85 90
cgc ccc gct atc tat gtg ccc tta gaa aaa tcc caa tat ttc tca ccg 1958
Arg Pro Ala Ile Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro
95 100 105
gcg gta ctc gaa aac tta gaa caa caa caa ttg gtt tgt tta gat aat 2006
Ala Val Leu Glu Asn Leu Glu Gln Gln Leu Val Cys Leu Asp Asn
110 115 120
tta cag gca att ata ggc aat act gaa tgg gaa tta gcg att ttt gat 2054
Leu Gln Ala Ile Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp
125 130 135 140
tta ttt aat cgc ata aaa tct gtt gaa aat aca ctg ctt gtg atc agt 2102
Leu Phe Asn Arg Ile Lys Ser Val Glu Asn Thr Leu Leu Val Ile Ser
145 150 155
gca aat caa tcc cca act gca tta cct gta agt tta cct gac tta gct 2150
Ala Asn Gln Ser Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala
160 165 170
tca cgt tta cgc tgg gga gaa agc tat cag ctg gtc ccc tta aat gat 2198
Ser Arg Leu Arg Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp
175 180 185

caa caa aaa atc cat gta ttg caa aaa aat gca cat caa cgt ggt atc	2246
Gln Gln Lys Ile His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile	
190 195 200	
gaa ctc ccc gat gaa gta gct aat ttt ctt ttg aaa cgc tta gag cgc	2294
Glu Leu Pro Asp Glu Val Ala Asn Phe Leu Leu Lys Arg Leu Glu Arg	
205 210 215 220	
gat atg aaa acg tta ttt gaa gca cta agt aaa tta gat aaa gca tca	2342
Asp Met Lys Thr Leu Phe Glu Ala Leu Ser Lys Leu Asp Lys Ala Ser	
225 230 235	
tta caa gcc caa cgt aaa tta acg att ccc ttt gta aaa gaa att tta	2390
Leu Gln Ala Gln Arg Lys Leu Thr Ile Pro Phe Val Lys Glu Ile Leu	
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Lys Leu	

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<212> PRT
<213> Pasteurella multocida

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20 25 30	
His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr Pro Asp Asn Asn	
35 40 45	
Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr Cys Leu Thr Gln	
50 55 60	
Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly Lys Ser His Leu	
65 70 75 80	
Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln Arg Pro Ala Ile	
85 90 95	
Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro Ala Val Leu Glu	
100 105 110	
Asn Leu Glu Gln Gln Leu Val Cys Leu Asp Asn Leu Gln Ala Ile	
115 120 125	
Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp Leu Phe Asn Arg	
130 135 140	
Ile Lys Ser Val Glu Asn Thr Leu Leu Val Ile Ser Ala Asn Gln Ser	
145 150 155 160	
Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala Ser Arg Leu Arg	
165 170 175	
Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp Gln Gln Lys Ile	
180 185 190	

His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile Glu Leu Pro Asp
195 200 205

Glu Val Ala Asn Phe Leu Leu Lys Arg Leu Glu Arg Asp Met Lys Thr
210 215 220

Leu Phe Glu Ala Leu Ser Lys Leu Asp Lys Ala Ser Leu Gln Ala Gln
225 230 235 240

Arg Lys Leu Thr Ile Pro Phe Val Lys Glu Ile Leu Lys Leu
245 250

<210> 11
<211> 2060
<212> DNA
<213> Pasteurella multocida

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<222> (856) .. (1389)

<220>
<223> dsbB

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tggggcatct tggcaaagtt tgatcgcaat aatcaacaaa aaatgtcacg acaagatcgt 180
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ctcgccgccc tcggtatcat tggtttaacg gtgattattt tggctacttc attttgttgt 300
gtcaccagcg agcatgctat tggtaaagcc tttcaggaat ctttaccctt cacagcattg 360
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aaagcggcat tagaggctgg cttaattgct caaccacaat atgaattact ggcagtagca 600
attaataccg gtaccaatct tccttctgtt gcaacccaa atggtcaagc cgcattctt 660
tttttattga cctcatcaact ggcaccatata attcgctttt cttatggtag aatggtttat 720
atggcattgc cttataccat cgtattatcc tgtattggtt tattgactgt ggaatataatt 780
ttgcctggcg caaccaatgt gctcattcaa attggtttat taaaaccaat gtaatgacaa 840
gtaaaaggag gaaac atg cta agc ttt ttt aag aca ctc tca aca aaa cga 891
Met Leu Ser Phe Phe Lys Thr Leu Ser Thr Lys Arg
1 5 10

agt gca tgg ttt cta ttg ttt agc tca gct tta cta gag gag gct atc 939
Ser Ala Trp Phe Leu Leu Phe Ser Ser Ala Leu Leu Leu Glu Ala Ile
15 20 25

gct ctt tat ttt caa cat ggc atg ggg ctc gcc cct tgt gtc atg tgt	987
Ala Leu Tyr Phe Gln His Gly Met Gly Leu Ala Pro Cys Val Met Cys	
30 35 40	
att tac gag agg gta gct att ctt ggc att gct ttc tcc ggt tta ttg	1035
Ile Tyr Glu Arg Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu	
45 50 55 60	
ggg tta ctc tac ccg agt tcg atg ctt ttg cgc ctt gtg gcg tta tta	1083
Gly Leu Leu Tyr Pro Ser Ser Met Leu Leu Arg Leu Val Ala Leu Leu	
65 70 75	
att ggt tta agc agt gca atc aaa ggc tta atg att agc atc acc cat	1131
Ile Gly Leu Ser Ser Ala Ile Lys Gly Leu Met Ile Ser Ile Thr His	
80 85 90	
tta gat cta caa ctt tac cct gca cct tgg aaa caa tgt tca gcg gtg	1179
Leu Asp Leu Gln Leu Tyr Pro Ala Pro Trp Lys Gln Cys Ser Ala Val	
95 100 105	
gca gaa ttt ccc gag act tta ccc tta gat cag tgg ttt cct gca ctc	1227
Ala Glu Phe Pro Glu Thr Leu Pro Leu Asp Gln Trp Phe Pro Ala Leu	
110 115 120	
ttc ctc cct tca ggc tca tgc agt gaa gta aca tgg caa ttt ctc ggc	1275
Phe Leu Pro Ser Gly Ser Cys Ser Glu Val Thr Trp Gln Phe Leu Gly	
125 130 135 140	
ttt tct atg gtg caa tgg atc gtc gtc att ttt gca ctc tat acc tta	1323
Phe Ser Met Val Gln Trp Ile Val Val Ile Phe Ala Leu Tyr Thr Leu	
145 150 155	
tta ctt gct ctc att ttc atc agc caa gtc aaa cgt cta aaa ccc aag	1371
Leu Leu Ala Leu Ile Phe Ile Ser Gln Val Lys Arg Leu Lys Pro Lys	
160 165 170	
cag cgc aga ctc ttt cat taagtcataa aaaatggtgc gataaagcac	1419
Gln Arg Arg Leu Phe His	
175	
cattttcat ttctcggtcg gtatagatta aatttcttgc acgacaaaact gcaggaaatg	1479
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gctcatcttc tttaatcgta tcaggcattt gcgtataag ccaatgtaaa tattctgaac	2019
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<210> 12
<211> 178
<212> PRT
<213> Pasteurella multocida

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Gln His Gly Met Gly Leu Ala Pro Cys Val Met Cys Ile Tyr Glu Arg
35 40 45

Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu Gly Leu Leu Tyr
50 55 60

Pro Ser Ser Met Leu Leu Arg Leu Val Ala Leu Leu Ile Gly Leu Ser
65 70 75 80

Ser Ala Ile Lys Gly Leu Met Ile Ser Ile Thr His Leu Asp Leu Gln
85 90 95

Leu Tyr Pro Ala Pro Trp Lys Gln Cys Ser Ala Val Ala Glu Phe Pro
100 105 110

Glu Thr Leu Pro Leu Asp Gln Trp Phe Pro Ala Leu Phe Leu Pro Ser
115 120 125

Gly Ser Cys Ser Glu Val Thr Trp Gln Phe Leu Gly Phe Ser Met Val
130 135 140

Gln Trp Ile Val Val Ile Phe Ala Leu Tyr Thr Leu Leu Leu Ala Leu
145 150 155 160

Ile Phe Ile Ser Gln Val Lys Arg Leu Lys Pro Lys Gln Arg Arg Leu
165 170 175

Phe His

<210> 13
<211> 4426
<212> DNA
<213> Pasteurella multocida

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<222> (2756) . . . (3211)

<220>
<223> exbB

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gacttcacgt agcggttcct taatattgtc atcagttaaa cgtccacgtc cactaatgtt 180
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tga

6876

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Glu Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu
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Thr Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn
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Val Ser Tyr Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg
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Lys Val Glu Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn
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Phe Ser Pro Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu
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Lys Val Pro Leu Leu Gly Val Ser Ser Pro Ser Ser Tyr Ser Glu His
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1890 1895 1900

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tcttttaat ctcttttaag tttaggatt aacttaat atg aac aaa aat cgt tac 1496
Met Asn Lys Asn Arg Tyr
1 5

aaa ctc att ttt agt caa gtc aaa ggt tgt ctc gtt cct gtg gca gaa 1544
Lys Leu Ile Phe Ser Gln Val Lys Gly Cys Leu Val Pro Val Ala Glu
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Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser Ser Asp Ser Thr Ser Thr
25 30 35

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Ser Glu Gln Val Glu Glu Pro Phe Leu Leu Glu Gln Tyr Ser Leu
40 45 50

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Ser Ser Val Ser Leu Leu Val Lys Ser Thr Phe Asn Pro Val Ser Tyr
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Ala Met Gln Leu Thr Trp Lys Gln Leu Ser Ile Leu Phe Leu Thr Val
75 80 85

att tct gtt cct gtt ttg gct gag gga aaa ggg gat gaa aga aat caa 1784
Ile Ser Val Pro Val Leu Ala Glu Gly Lys Gly Asp Glu Arg Asn Gln
90 95 100

tta aca gtg att gat aat agc gat cat att aaa tta gat gca tct aat 1832
Leu Thr Val Ile Asp Asn Ser Asp His Ile Lys Leu Asp Ala Ser Asn
105 110 115

ctt gct ggt aat gat aaa aca aaa atc tat caa gca gaa aat aaa gtt 1880
Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr Gln Ala Glu Asn Lys Val
120 125 130

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gtg aca ggt cct caa gaa agt aaa att gtt ggc gcg ctt gaa gta tta Val Thr Gly Pro Gln Glu Ser Lys Ile Val Gly Ala Leu Glu Val Leu 200 205 210	2120
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gag ctt ata gat ccg aat cag atg atg tta aag gtt aca aaa gga aat Glu Leu Ile Asp Pro Asn Gln Met Met Leu Lys Val Thr Lys Gly Asn 250 255 260	2264
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gta tct aat gat gtt att gct atc acg gga tct agt aca ggc gca atg Val Ser Asn Asp Val Ile Ala Ile Thr Gly Ser Ser Thr Gly Ala Met 330 335 340	2504
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aaa cat gat gga att att ttg tct gaa aat gat att cag att gaa atg Lys His Asp Gly Ile Ile Leu Ser Glu Asn Asp Ile Gln Ile Glu Met 360 365 370	2600
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tta gag gcg aaa caa gtt aaa atc aga aaa aac gca gag att agg agt Leu Glu Ala Lys Gln Val Lys Ile Arg Lys Asn Ala Glu Ile Arg Ser 425 430 435	2792
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act aat gct ggg cgt att tat ggt cga gag gtt aag ctt gac act aat Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu Val Lys Leu Asp Thr Asn 475 480 485	2936
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cca ctg atg cgc gta aaa agt agt gtc cgc ttt tta ggc tct ccg ttt Pro Leu Met Arg Val Lys Ser Ser Val Arg Phe Leu Gly Ser Pro Phe 520 525 530	3080
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cct ggt ttt gtg aat aag gga ctc att gaa agt gcg ggg agt gca gaa Pro Gly Phe Val Asn Lys Gly Leu Ile Glu Ser Ala Gly Ser Ala Glu 555 560 565	3176
tta act ttt aaa gaa aaa acc agt ttt tta aca gag ggc aat aat ttt Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu Thr Glu Gly Asn Asn Phe 570 575 580	3224
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<213> Pasteurella multocida

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20 25 30

Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu
35 40 45

Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
50 55 60

Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
65 70 75 80

Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys
85 90 95

Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile
100 105 110

Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr
115 120 125

Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly
130 135 140

Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
145 150 155 160

Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu
165 170 175

Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala
180 185 190

Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val
195 200 205

Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn
210 215 220

Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg
225 230 235 240

Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu
245 250 255

Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr
260 265 270

Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys
275 280 285

Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr
290 295 300

Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys
305 310 315 320

Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly
325 330 335

Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr
340 345 350

Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn
355 360 365

Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr
370 375 380

Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys
385 390 395 400

Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr
405 410 415

Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys
420 425 430

Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly
435 440 445

Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp
450 455 460

Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu
465 470 475 480

Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala
485 490 495

Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile
500 505 510

Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg
515 520 525

Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser
530 535 540

Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu
545 550 555 560

Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu
565 570 575

Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu
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<222> (1)..(1446)

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cat gct tac caa aac cag ccc cta tca aca aaa gtt gtt ttt caa tta	96
His Ala Tyr Gln Asn Gln Pro Leu Ser Thr Lys Val Val Phe Gln Leu	
20 25 30	
gtg aaa gat ttg acg gaa gtt tta tac cgt tct ggc tac gtg aca agt	144
Val Lys Asp Leu Thr Glu Val Leu Tyr Arg Ser Gly Tyr Val Thr Ser	
35 40 45	
gca att ggt tta aaa aat tca aaa atc agc aat ggc gat ctt gaa ttt	192
Ala Ile Gly Leu Lys Asn Ser Lys Ile Ser Asn Gly Asp Leu Glu Phe	
50 55 60	
att gta ctg tgg gga aga act cgc gat ctg ttt gtg aat ggg gag aaa	240
Ile Val Leu Trp Gly Arg Thr Arg Asp Leu Phe Val Asn Gly Glu Lys	
65 70 75 80	
cca acc cgt ttt aga gat aaa aca atg tta tca gtc cta ccc aat tta	288
Pro Thr Arg Phe Arg Asp Lys Thr Met Leu Ser Val Leu Pro Asn Leu	
85 90 95	
atc gga aat cgc tta agt att cac gac att gac cag ttg atc gaa atc	336
Ile Gly Asn Arg Leu Ser Ile His Asp Ile Asp Gln Leu Ile Glu Ile	
100 105 110	
tta aat act acg aat aaa aaa gcc aca gtg aat gtg gtt gca agt gaa	384
Leu Asn Thr Thr Asn Lys Lys Ala Thr Val Asn Val Val Ala Ser Glu	
115 120 125	
gaa aaa ggc agc tca aat cta aat att gaa aga caa tat gat gtt ttt	432
Glu Lys Gly Ser Ser Asn Leu Asn Ile Glu Arg Gln Tyr Asp Val Phe	
130 135 140	
ccg caa gtg agt gtc gga ttc aat aat tca ggt gct ggc aat aat gcc	480
Pro Gln Val Ser Val Gly Phe Asn Asn Ser Gly Ala Gly Asn Asn Ala	
145 150 155 160	
aat ggg cgt aat caa gct aca ttg aat att gct tgg agt gat cta tta	528
Asn Gly Arg Asn Gln Ala Thr Leu Asn Ile Ala Trp Ser Asp Leu Leu	
165 170 175	
ggc acg aat gat cgt tgg agt ttc tcg agt agt tac cgt tta tat aaa	576
Gly Thr Asn Asp Arg Trp Ser Phe Ser Ser Tyr Arg Leu Tyr Lys	
180 185 190	
aat cat cat gct aac cag caa cgc aat tat act ttg tct tac agt cag	624
Asn His His Ala Asn Gln Gln Arg Asn Tyr Thr Leu Ser Tyr Ser Gln	
195 200 205	
cct ata ggc ttt tct aca gta gaa att aaa gca tcg gaa tct acg tat	672
Pro Ile Gly Phe Ser Thr Val Glu Ile Lys Ala Ser Glu Ser Thr Tyr	
210 215 220	
gaa aaa gaa ctt cgc ggt ata aat act cat tct tct cat ggg aaa acc	720
Glu Lys Glu Leu Arg Gly Ile Asn Thr His Ser Ser His Gly Lys Thr	
225 230 235 240	
caa agc tta gct gtc aag ctg atg cat gtg tta ttg cgt aat aag gag	768
Gln Ser Leu Ala Val Lys Leu Met His Val Leu Leu Arg Asn Lys Glu	
245 250 255	
agt att tta tct aca tat acc gag ttc gag ttt aaa aaa cgg att agt	816
Ser Ile Leu Ser Thr Tyr Thr Glu Phe Glu Phe Lys Lys Arg Ile Ser	
260 265 270	

tat ttt tct gat att ttg att ggg aaa tat cac aat aat aaa gtg agc 864
Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser
275 280 285

gta ggg tta tct tac atg act aat ttt gct tac ggg aag ctt tac agc 912
Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser
290 295 300

gac att gct tac gcg aat ggg ttg aga tgg ttt ggg gcg aat tat tca 960
Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser
305 310 315 320

gca tat gat gca aat cgt gaa aaa acc tta aaa tta ttg tca gga agt 1008
Ala Tyr Asp Ala Asn Arg Glu Lys Thr Leu Lys Leu Leu Ser Gly Ser
325 330 335

att aat tgg cag cgt cca ata tcc ctg ttt gaa cgt gcg atg aat tat 1056
Ile Asn Trp Gln Arg Pro Ile Ser Leu Phe Glu Arg Ala Met Asn Tyr
340 345 350

caa tta cgt att ggt gcc caa tat ggt ttt gat agt ttg tat tct gaa 1104
Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu
355 360 365

aat caa ttt tca att ggt gat gaa tat aca gta aga gga ttt aaa ggt 1152
Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly
370 375 380

ggt gcg gtt tct ggt gat agt ggt gcg tat tta tca caa aca ctg acg 1200
Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr
385 390 395 400

gtt cct ttt tat cca caa aaa gca tat tta tct cag gta tcc cct ttt 1248
Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe
405 410 415

att gga ttt gat atg ggt aaa gta cat att aaa tca aag cat aaa aca 1296
Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr
420 425 430

acc act tta gtc ggt ttt gcc cta ggc ttg aaa acg caa ata aag tta 1344
Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu
435 440 445

ttt tca tta tca tta acc tat gca caa cca atg aat ggt gtg agt ggt 1392
Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly
450 455 460

gtt acg caa cat cgt caa aaa ccg att tat tat ttc tca gga tca ctt 1440
Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu
465 470 475 480

tct ttt taatctcttt taagtttaag gattaactta atatgaacaa aaatcggtac 1496
Ser Phe

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Val Lys Asp Leu Thr Glu Val Leu Tyr Arg Ser Gly Tyr Val Thr Ser
35 40 45

Ala Ile Gly Leu Lys Asn Ser Lys Ile Ser Asn Gly Asp Leu Glu Phe
50 55 60

Ile Val Leu Trp Gly Arg Thr Arg Asp Leu Phe Val Asn Gly Glu Lys
65 70 75 80

Pro Thr Arg Phe Arg Asp Lys Thr Met Leu Ser Val Leu Pro Asn Leu
85 90 95

Ile Gly Asn Arg Leu Ser Ile His Asp Ile Asp Gln Leu Ile Glu Ile
100 105 110

Leu Asn Thr Thr Asn Lys Lys Ala Thr Val Asn Val Val Ala Ser Glu
115 120 125

Glu Lys Gly Ser Ser Asn Leu Asn Ile Glu Arg Gln Tyr Asp Val Phe
130 135 140

Pro Gln Val Ser Val Gly Phe Asn Asn Ser Gly Ala Gly Asn Asn Ala
145 150 155 160

Asn Gly Arg Asn Gln Ala Thr Leu Asn Ile Ala Trp Ser Asp Leu Leu
165 170 175

Gly Thr Asn Asp Arg Trp Ser Phe Ser Ser Ser Tyr Arg Leu Tyr Lys
180 185 190

Asn His His Ala Asn Gln Gln Arg Asn Tyr Thr Leu Ser Tyr Ser Gln
195 200 205

Pro Ile Gly Phe Ser Thr Val Glu Ile Lys Ala Ser Glu Ser Thr Tyr
210 215 220

Glu Lys Glu Leu Arg Gly Ile Asn Thr His Ser Ser His Gly Lys Thr
225 230 235 240

Gln Ser Leu Ala Val Lys Leu Met His Val Leu Leu Arg Asn Lys Glu
245 250 255

Ser Ile Leu Ser Thr Tyr Thr Glu Phe Glu Phe Lys Lys Arg Ile Ser
260 265 270

Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser
275 280 285

Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser
290 295 300

Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser
305 310 315 320

Ala Tyr Asp Ala Asn Arg Glu Lys Thr Leu Lys Leu Leu Ser Gly Ser
325 330 335

Ile Asn Trp Gln Arg Pro Ile Ser Leu Phe Glu Arg Ala Met Asn Tyr
340 345 350

Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu
355 360 365

Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly
370 375 380

Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr
385 390 395 400

Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe
405 410 415

Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr
420 425 430

Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu
435 440 445

Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly
450 455 460

Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu
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Ser Phe

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gtacgataag atcgccatgc atttcatgt ttttatttt tccattggtt aatagactgg 180
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caagatcaat ctcagcataa ctgaaatgac tgacgagtaa actacatata agtatcggtc 420
gtttgaaaag gcgtaaaagc gtggcagtaa aaaaagaaga tattttatac ataattggct 480
cgagcagttt ctatttttt attgtcgaaac aataatagta tttgaaccct cgagagtaaa 540
tcctttctc gttaaacact tatttttta ttcaactacg gcattgtttt tacaatgttg 600

tggtttgtt tttatctaaa aaggaagaaa aaacgatt atg aaa cag att cca atg 656
Met Lys Gln Ile Pro Met
1 5

act ata cgt ggt gcg gaa caa tta aga caa gaa ctc gat ttt ttg aaa 704
Thr Ile Arg Gly Ala Glu Gln Leu Arg Gln Glu Leu Asp Phe Leu Lys
10 15 20

aac act cgt cgc cca gaa att att aat gct atc gca gaa gct cgt gaa 752
Asn Thr Arg Arg Pro Glu Ile Ile Asn Ala Ile Ala Glu Ala Arg Glu
25 30 35

cat ggc gat cta aaa gaa aat gca gaa tac cat gct gcg cgt gaa cag 800
His Gly Asp Leu Lys Glu Asn Ala Glu Tyr His Ala Ala Arg Glu Gln
40 45 50

caa gga ttt tgt gaa gga cga atc caa gaa att gaa ggg aaa tta gcg 848
Gln Gly Phe Cys Glu Gly Arg Ile Gln Glu Ile Glu Gly Lys Leu Ala
55 60 65 70

aat agt caa att att gat gtc aca aag atc cca aat aat ggc aaa gtg 896
Asn Ser Gln Ile Ile Asp Val Thr Lys Ile Pro Asn Asn Gly Lys Val
75 80 85

att ttt ggt gcc aca att ttg tta ctg aat att gac acg gaa gaa gaa 944
Ile Phe Gly Ala Thr Ile Leu Leu Asn Ile Asp Thr Glu Glu Glu
90 95 100

gtc tcg tac caa att gta ggc gat gat gaa gcc aat att aaa gca ggg 992
Val Ser Tyr Gln Ile Val Gly Asp Asp Glu Ala Asn Ile Lys Ala Gly
105 110 115

cta att tca gtt aac gcc acg cga ttg aat tagagaaagc taaatggatt 1042
Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
120 125

gcccaagatc ttggcgtcaa acaaacgtta attgacactt ccgtcattaa agcgattacg 1102

caaaatgcct taatggacga acaggcaaga attgagcaac atggcagttac accgaatact 1162

ttcggttga 1170

<210> 22:
<211> 128
<212> PRT
<213> Pasteurella multocida

<400> 22
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1 5 10 15

Glu Leu Asp Phe Leu Lys Asn Thr Arg Arg Pro Glu Ile Ile Asn Ala
20 25 30

Ile Ala Glu Ala Arg Glu His Gly Asp Leu Lys Glu Asn Ala Glu Tyr
35 40 45

His Ala Ala Arg Glu Gln Gln Gly Phe Cys Glu Gly Arg Ile Gln Glu
50 55 60

Ile Glu Gly Lys Leu Ala Asn Ser Gln Ile Ile Asp Val Thr Lys Ile
65 70 75 80

Pro Asn Asn Gly Lys Val Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn
85 90 95

Ile Asp Thr Glu Glu Val Ser Tyr Gln Ile Val Gly Asp Asp Glu
100 105 110

Ala Asn Ile Lys Ala Gly Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
115 120 125

<210> 23
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 gcgatcaatt tattccgatc aatcggttgt aatacttcaa tcagctctgc ccaagggtga 180
 tcaatttgct gtgtttgttt tggaaaagac aaattaatgc caaagccaat cacgagatta 240
 tggattat tctgacgatt ggcgatttcg accaaaatcc ctgctaattt gcgcccattgt 300
 aatagcacat catttggcca ttttaatcca atgttcaaag cacctgcttg cttagcggtt 360
 tctgcgattt ccataccac tactaaactc aagccttcta aattgacctt ttggtcacat 420
 gcccaataca aactcataat cacttgtcca gcaaaaggag aaagccattt acgaccacgt 480
 cgtccacgatc ccgcagttt atattctgct aagcaaatag cgccttttc caaatgtgca 540
 atattgtcaa gcaagaattt attggtcgag ttaataatcg gcttaatata aagtggtaa 600
 ggtgctaacg cttgcgtcaa ataagattca tttaaagcgac ttaatttgcgatgagacga 660
 aatgttgaa cttgcgtttc tatttgtatc cttgttgtt tcaatttttc gatattgtgt 720
 aagatatactt gttctgaata acctaaaagt gcagtcaatt ctgctaaaga aagttgtga 780
 tagctagcga gtaatgcgaa tacgtttgc ataaaaatcc ttattttat aaccaaaagag 840
 aggcaactta ttatagacaa tgattttctc gaaaatcgat aaaaaatcc atttcaaac 900
 agcaacgaaa tctgtataat gcgaccgcaa tatttttac ctttttattt ttcatatcaa 960
 cctaagagag aatattgca atg tta cga gta ata aaa gaa gca tta acc ttc 1012
 Met Leu Arg Val Ile Lys Glu Ala Leu Thr Phe
 1 5 10
 gat gat gtt ttg ctt gtc cca gca cat tct act gtg ctc cca aat acc 1060
 Asp Asp Val Leu Leu Val Pro Ala His Ser Thr Val Leu Pro Asn Thr
 15 20 25

gca gac ctt tcc act caa ctc acc aaa act atc cgc ctc aat atc cca Ala Asp Leu Ser Thr Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro	1108
30 35 40	
atg tta tcc gcc gcc atg gat acc gtc aca gaa act aaa ctg gca atc Met Leu Ser Ala Ala Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile	1156
45 50 55	
tct ctt gca caa gaa ggt ggc atc ggg ttt att cat aaa aat atg tct Ser Leu Ala Gln Glu Gly Ile Gly Phe Ile His Lys Asn Met Ser	1204
60 65 70 75	
att gag cgt caa gcg gaa cgt gtc cgc aaa gtc aaa aat ttt gag agc Ile Glu Arg Gln Ala Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser	1252
80 85 90	
ggt att gta tcc gat cct gtc acc gtt tca cca acc tta tct tta gca Gly Ile Val Ser Asp Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala	1300
95 100 105	
gaa tta agt gaa tta gtg aag aaa aat ggt ttt gcg agt ttc cct gtt Glu Leu Ser Glu Leu Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val	1348
110 115 120	
gtt gat gat gaa aaa aat ctt gtc ggt atc att act ggt cgt gat aca Val Asp Asp Glu Lys Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr	1396
125 130 135	
cgc ttt gtc acg gat tta aat aaa aca gtc gcg gac ttt atg acc cct Arg Phe Val Thr Asp Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro	1444
140 145 150 155	
aaa gct cgt ctt gtc acg gtg aaa cgc aat gca agt cgc gat gaa att Lys Ala Arg Leu Val Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile	1492
160 165 170	
ttt ggt cta atg cat aca cac cgt gta gaa aaa gtc ctt gtt gtc agc Phe Gly Leu Met His Thr His Arg Val Glu Lys Val Leu Val Val Ser	1540
175 180 185	
gac gat ttc aaa tta aaa ggc atg atc acc tta aaa gac tac caa aaa Asp Asp Phe Lys Leu Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys	1588
190 195 200	
tcc gag caa aaa cca caa gcc tgt aaa gat gaa ttt ggt cgt tta cgt Ser Glu Gln Lys Pro Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg	1636
205 210 215	
gtc ggt gct gca gta gga gca gga cct ggt aat gaa gaa cgt att gat Val Gly Ala Ala Val Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp	1684
220 225 230 235	
gca tta gtg aaa gca ggg gtc gat gtg tta ttg att gac tca tca cac Ala Leu Val Lys Ala Gly Val Asp Val Leu Leu Ile Asp Ser Ser His	1732
240 245 250	
ggt cat tca gaa ggt gtg tta caa cgt gtg cgt gaa act cgt gcg aaa Gly His Ser Glu Gly Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys	1780
255 260 265	
tac cca gat ttg cca att gtt gca ggt aat gtg gca acc gct gaa ggc Tyr Pro Asp Leu Pro Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly	1828
270 275 280	

gca att gcg ttg gct gat gca ggg gca agt gca gtg aaa gtg ggg att 1876
Ala Ile Ala Leu Ala Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile
285 290 295

ggt cct ggt tca att tgt aca aca cgt att gtc aca ggc gtg ggc gtt 1924
Gly Pro Gly Ser Ile Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val
300 305 310 315

cca caa att aca gcg att gcc gat gcg gca gaa gca cta aaa gat cgg 1972
Pro Gln Ile Thr Ala Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg
320 325 330

ggt att cct gtg att gca gat ggc ggt atc cgt ttc tct ggt gat att 2020
Gly Ile Pro Val Ile Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile
335 340 345

tcg aaa gcc att gcg gcg ggc gcc tct tgt gtt atg gtg ggt tcc atg 2068
Ser Lys Ala Ile Ala Ala Gly Ala Ser Cys Val Met Val Gly Ser Met
350 355 360

ttt gca ggt aca gaa gaa gca cca ggt gaa atc gaa ctt tat caa ggt 2116
Phe Ala Gly Thr Glu Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly
365 370 375

cgt gcc ttt aaa tct tat cga ggt atg gga tcg tta ggt gcg atg agc 2164
Arg Ala Phe Lys Ser Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser
380 385 390 395

aaa ggc tca agc gac cgc tat ttc cag tcc gat aat gca gct gac aaa 2212
Lys Gly Ser Ser Asp Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys
400 405 410

tta gta cca gaa ggt att gaa gga cgt att cca tat aaa gga ttc tta 2260
Leu Val Pro Glu Gly Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu
415 420 425

aaa gaa att atc cat caa caa atg ggt gga ttg cgt tct tgt atg ggc 2308
Lys Glu Ile Ile His Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly
430 435 440

tta acg ggt tgt gca acc att gat gaa ctc cgt acc aaa gcg cag ttt 2356
Leu Thr Gly Cys Ala Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe
445 450 455

gtg cgc att agt ggt gca ggg atc caa gaa agc cat gtg cat gat gtg 2404
Val Arg Ile Ser Gly Ala Gly Ile Gln Glu Ser His Val His Asp Val
460 465 470 475

act atc aca aaa gaa gcc cct aat tat cgt atg ggt taaacattgc 2450
Thr Ile Thr Lys Glu Ala Pro Asn Tyr Arg Met Gly
480 485

ttaggtgggg attatccccca cctaagttta ttttaataa caacgttaat agagaagctt 2510
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tatatagagg atgtttaaaa aaccgataac atcttgatgt catcgcaat tcaaactcct 3830
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acccagttga ttgcccgcg tgtacgtgaa attggcgtgt actgcgaact ttggcatgg 4010
gatgtatccg aagccgatat tcgtgagttt aatccaaactg ggattattct ttctgggt 4070
cctgaaagta ccactgaaga aaacagccca cgagctcccg aatacgtatt caacgcccgt 4130
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cacccagaag tgactcatac aaaaagcggtt cttaattttaacgaaattt tgggtgaag 4490
atctgtgggtt gtgaacgtaa ctggacacca gaaaatatac ttgaagatgc cggtgctcgt 4550
cttaaaggcac aagtgggcga tggatgaaatg attttaggct tatctgggtt cgtaactgc 4610
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<211> 487
<212> PRT
<213> Pasteurella multocida

<400> 24
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Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr
20 25 30
Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala
35 40 45
Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu
50 55 60
Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala
65 70 75 80
Glu Arg Val Arg Lys Val Lys Phe Glu Ser Gly Ile Val Ser Asp
85 90 95
Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala Glu Leu Ser Glu Leu
100 105 110
Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val Val Asp Asp Glu Lys
115 120 125
Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp
130 135 140
Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro Lys Ala Arg Leu Val
145 150 155 160
Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile Phe Gly Leu Met His
165 170 175
Thr His Arg Val Glu Lys Val Leu Val Val Ser Asp Asp Phe Lys Leu
180 185 190
Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ser Glu Gln Lys Pro
195 200 205
Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val
210 215 220
Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala
225 230 235 240
Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly
245 250 255
Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro
260 265 270
Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala
275 280 285
Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile
290 295 300

Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala
305 310 315 320

Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg Gly Ile Pro Val Ile
325 330 335

Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile Ser Lys Ala Ile Ala
340 345 350

Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu
355 360 365

Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser
370 375 380

Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp
385 390 395 400

Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly
405 410 415

Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu Lys Glu Ile Ile His
420 425 430

Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala
435 440 445

Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe Val Arg Ile Ser Gly
450 455 460

Ala Gly Ile Gln Glu Ser His Val His Asp Val Thr Ile Thr Lys Glu
465 470 475 480

Ala Pro Asn Tyr Arg Met Gly
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<210> 25
<211> 2364
<212> DNA
<213> *Pasteurella multocida*

<220>
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<222> (191)..(1828)

<220>
<223> Hi1501

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tgcgctagag atgctgtgga aaaatgcgggt aagcagctct gccccgattt agttcatgac 120
aattgacggc gattttagggc gtgatgaatt tgatgacggc gatttataaca gtatttggcg 180
gagataaaaa atg gcg aag aaa aag aaa aaa tta caa caa gcg aaa aaa 229
Met Ala Lys Lys Lys Lys Leu Gln Gln Ala Lys Lys
1 5 10

gta caa gtt ggc tta gat aca caa aca aat gag gcg cgt gtc acg gag 277
Val Gln Val Gly Leu Asp Thr Gln Thr Asn Glu Ala Arg Val Thr Glu
15 20 25

aca gga aga att att tct gat cac cca agc aat aaa att acc ccc gca	325
Thr Gly Arg Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala	
30 35 40 45	
aag tta aaa ggg att tta gaa gat gct gaa ggt ggt gat att acc gcg	373
Lys Leu Lys Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala	
50 55 60	
caa cat gag ctt ttc atg gat att gaa gaa cgc gac agt tgc atc ggg	421
Gln His Glu Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly	
65 70 75	
gca aat att caa acc cgt aag cgt gcg att tta acc ctt gac tgg cgc	469
Ala Asn Ile Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg	
80 85 90	
att gca gag cca cgt aat gcc aca ccg caa gaa gaa aaa ctg caa gtc	517
Ile Ala Glu Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val	
95 100 105	
gaa att gac gag ctt ttc tat caa ttc cca atg cta gaa gat tta atg	565
Glu Ile Asp Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met	
110 115 120 125	
gtg gat atg atg gat gcg gta gga cat ggt ttt tcg gcg tta gaa att	613
Val Asp Met Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile	
130 135 140	
gaa tgg aag caa gct gaa agt aaa tgg att cca gtt aat ttt atc gca	661
Glu Trp Lys Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala	
145 150 155	
cgt ccg cag tcg tgg ttt aaa cta gac aag gat gat aat tta ctg ctt	709
Arg Pro Gln Ser Trp Phe Lys Leu Asp Lys Asp Asp Asn Leu Leu Leu	
160 165 170	
aaa acg cca gat aat caa gac ggt gag ccg ttg aga caa tat ggc tgg	757
Lys Thr Pro Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp	
175 180 185	
gta gtg cat acc cac aaa tca aga aca gta cag ctt gct cgt atg ggt	805
Val Val His Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly	
190 195 200 205	
tta ttt aga acg ctc gca tgg ctt tat atg ttt aaa cac tac tcg gtg	853
Leu Phe Arg Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val	
210 215 220	
cat gat ttt gcc gaa ttt cta gag ctt tat ggt atg ccg att cgt att	901
His Asp Phe Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile	
225 230 235	
ggt aaa tac cca ttt ggg gca acg aat gac gaa aag cgc aca tta ttg	949
Gly Lys Tyr Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu	
240 245 250	
cgt gca ctt gct caa atc gga cat aac gca gca ggg att atg cca gaa	997
Arg Ala Leu Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu	
255 260 265	
gga atg aat gtt gag ttg cat aat gtg aca aac act act ggc tcg gct	1045
Gly Met Asn Val Glu Leu His Asn Val Thr Asn Thr Thr Gly Ser Ala	
270 275 280 285	

gga agc aac ccg ttt ttg caa atg gtg gac tgg tgt gaa aag tcc gcc Gly Ser Asn Pro Phe Leu Gln Met Val Asp Trp Cys Glu Lys Ser Ala 290 295 300	1093
gca cgt ttg att cta ggg caa aca tta aca agc ggt gca gat ggt aaa Ala Arg Leu Ile Leu Gly Gln Thr Leu Thr Ser Gly Ala Asp Gly Lys 305 310 315	1141
act tca act aat gcc ctt gga caa gtg cat aat gaa gtc aga cgt gac Thr Ser Thr Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp 320 325 330	1189
ttg ctt gtg tct gat gct aaa cag att gca caa act att aca caa cag Leu Leu Val Ser Asp Ala Lys Gln Ile Ala Gln Thr Ile Thr Gln Gln 335 340 345	1237
att att ctg cca tat ctt caa att aac att gat ccg aat att ttg cct Ile Ile Leu Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro 350 355 360 365	1285
tct cgt gtg ccg tat ttc gag ttt gac acg aaa gaa tat gct gat tta Ser Arg Val Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu 370 375 380	1333
agt gtc cta gcg gat gct att cct aag ctt gtg agc gta gga gtg cgc Ser Val Leu Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg 385 390 395	1381
att cct gaa aat tgg gtg cgt gat aaa gcg ggc att cca gaa ccg cag Ile Pro Glu Asn Trp Val Arg Asp Lys Ala Gly Ile Pro Glu Pro Gln 400 405 410	1429
gaa aat gaa acg att tta agt gcg gtt caa cat gat ttt aaa aca gat Glu Asn Glu Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp 415 420 425	1477
tta aac gat gtt gaa aat ccg aaa aaa cag acc gca ctt tct gta caa Leu Asn Asp Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln 430 435 440 445	1525
aat cac gtg aca ggt tgt cag tgt gat ggc tgt cgt ggt gtt gca tta Asn His Val Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu 450 455 460	1573
tct gcg aat aat aac agt tct act gcg cag ggc gtg cta gat ggt gga Ser Ala Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly 465 470 475	1621
ctt gcg caa gca ttt aat gag cct gat ttt aat aaa caa tta aat cca Leu Ala Gln Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro 480 485 490	1669
atg gta aag aaa gct gtt gcg gta ctc atg gca tgt gac tct tac gat Met Val Lys Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp 495 500 505	1717
gag gcg gca gaa aaa ctc gct gaa gca tac cca gaa att tca agt cac Glu Ala Ala Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His 510 515 520 525	1765
gaa cac gaa cag tat ctc tca aat gcg ctg ttt tta gct gat tta ctt Glu His Glu Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu 530 535 540	1813

gga gga act aat gtc taaaccgctt agttttctat tcggacttga accaacgcaa 1868
Gly Gly Thr Asn Val
545

gccattgagt ttttacataa taaaaaatta cttgcaacga aagtgtttaa aaaatcactg 1928
catgatagtg ccatcgcaag agctacaaca atcgcgagat tatctagtct tgagatgacg 1988
aatgatattt ataaatcaat ggaagttgcc aaaaaagagg gtaagagctt tacacaatgg 2048
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cgctatcagc gcatgatgga taatattgat catcgccct attggcaata ttccgctgtc 2288
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gaccgggtttt ggtcgaa 2364

<210> 26
<211> 546
<212> PRT
<213> Pasteurella multocida

<400> 26
Met Ala Lys Lys Lys Lys Lys Leu Gln Gln Ala Lys Lys Val Gln Val
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Gly Leu Asp Thr Gln Thr Asn Glu Ala Arg Val Thr Glu Thr Gly Arg
20 25 30

Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala Lys Leu Lys
35 40 45

Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala Gln His Glu
50 55 60

Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly Ala Asn Ile
65 70 75 80

Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg Ile Ala Glu
85 90 95

Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val Glu Ile Asp
100 105 110

Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met Val Asp Met
115 120 125

Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile Glu Trp Lys
130 135 140

Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala Arg Pro Gln
145 150 155 160

Ser Trp Phe Lys Leu Asp Lys Asp Asp Asn Leu Leu Leu Lys Thr Pro
165 170 175

Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp Val Val His

	180	185	190
Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly Leu Phe Arg			
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Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val His Asp Phe			
210	215	220	
Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile Gly Lys Tyr			
225	230	235	240
Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu Arg Ala Leu			
245	250	255	
Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu Gly Met Asn			
260	265	270	
Val Glu Leu His Asn Val Thr Asn Thr Thr Gly Ser Ala Gly Ser Asn			
275	280	285	
Pro Phe Leu Gln Met Val Asp Trp Cys Glu Lys Ser Ala Ala Arg Leu			
290	295	300	
Ile Leu Gly Gln Thr Leu Thr Ser Gly Ala Asp Gly Lys Thr Ser Thr			
305	310	315	320
Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp Leu Leu Val			
325	330	335	
Ser Asp Ala Lys Gln Ile Ala Gln Thr Ile Thr Gln Gln Ile Ile Leu			
340	345	350	
Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro Ser Arg Val			
355	360	365	
Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu Ser Val Leu			
370	375	380	
Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg Ile Pro Glu			
385	390	395	400
Asn Trp Val Arg Asp Lys Ala Gly Ile Pro Glu Pro Gln Glu Asn Glu			
405	410	415	
Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp Leu Asn Asp			
420	425	430	
Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln Asn His Val			
435	440	445	
Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu Ser Ala Asn			
450	455	460	
Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly Leu Ala Gln			
465	470	475	480
Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro Met Val Lys			
485	490	495	
Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp Glu Ala Ala			
500	505	510	
Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His Glu His Glu			

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Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu Gly Gly Thr
530 535 540

Asn Val
545

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<222> (2)...(1351)

<220>
<223> Nucleotides at positions 375, 399, 423, and 453
are A, T, C or G. The corresponding amino acids
are unknown.

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ttt tta gaa gat cgc cgt gaa aag aag ctt acc gaa gaa aaa aca tta 97
Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu
20 25 30

ggg ctt agt gat gca gtg cgt ttt gct aat gat caa acc cct tat ctc 145
Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu
35 40 45

cgt tat ggt att gaa tat cga tat aac ggc ttg tct tgg ttg gaa acg 193
Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr
50 55 60

gta aag ctt ttt ttg gca aag cag aaa atc gaa caa cgt tct gct ctc 241
Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
65 70 75 80

caa gag ttt gat att aat aat agg aat aaa ttg gat tcg act atg tcg 289
Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser
85 90 95

ttt gta tat tta caa aga cag aat ata gct cgg gga gaa ttt tca acg 337
Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr
100 105 110

agt cct tta tat tgg ggg ccg agt cgc cat cgt tta tnt gcg aaa ttc 385
Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe
115 120 125

gaa ttt cgt gat ang ttt tta gaa aat atg aat aag ctt ttt acg ttt 433
Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe
130 135 140

cgg ccg tgg caa atc aat ana ttc aga caa caa ggt cga aat aac tat	481
Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr	
145 150 155 160	
aca gaa gtg ttt ccc gtt aaa tcc cga gag ttt tct ttt tct ctt atg	529
Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met	
165 170 175	
gac gac att aag att ggc gaa ttg cta cat ctc gga ttg ggc ggt cgg	577
Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg	
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tgg gat cac tat aac tat aag cca tta tta aat tct cag cat aat atc	625
Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile	
195 200 205	
aac agg aca cag aga tta cct tat cca aaa aca tca tcc aaa ttt tcg	673
Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser	
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Tyr Gln Leu Ser Leu Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala	
225 230 235 240	
tac cgt tta agt acc ggt ttt agg gtt ccc cgt gtt gaa gat ctt tat	769
Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr	
245 250 255	
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Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp	
260 265 270	
cta caa ccg gaa act gca ctg aat cat gaa ata agt tac cgt ttc caa	865
Leu Gln Pro Glu Thr Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln	
275 280 285	
aat caa tat gcc cat ttc agc gtc ggg ctt ttc cgt aca cgt tat cat	913
Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His	
290 295 300	
aac ttt att caa gaa cgt gag atg acc tgt gat aaa att cca tat gag	961
Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu	
305 310 315 320	
tat aat agg act tat gga tat tgc acg cat aat act tat gta atg ttt	1009
Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe	
325 330 335	
gtt aat gaa cct gaa gcc gtg att aaa ggg gtt gaa gta agc ggt gct	1057
Val Asn Glu Pro Glu Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala	
340 345 350	
tta aat ggg tcg gca ttc gga ctt tcc gac ggt tta act ttc cgt ctc	1105
Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu	
355 360 365	
aaa ggg agc tac agc aaa ggt caa aat cat gac ggc gat ccg tta aaa	1153
Lys Gly Ser Tyr Ser Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys	
370 375 380	
tct att caa cca tgg aca gtg gta acc ggt att gat tac gaa act gaa	1201
Ser Ile Gln Pro Trp Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu	
385 390 395 400	

ggg tgg agc gtg agt ttg agc ggg cgt tat agt gcg gct aaa aaa gcc	1249
Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala	
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aaa gat gcg ata gaa acg gaa tac aca cat gat aaa aag gtt gtc aaa	1297
Lys Asp Ala Ile Glu Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys	
420 425 430	
caa tgg ccg cat tta agt cca tcc tac ttt gtt gat ttt acg ggg	1345
Gln Trp Pro His Leu Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly	
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Gln Val	
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Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu	
35 40 45	
Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr	
50 55 60	
Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu	
65 70 75 80	
Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser	
85 90 95	
Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr	
100 105 110	
Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe	
115 120 125	
Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe	
130 135 140	
Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr	
145 150 155 160	
Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met	
165 170 175	
Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Arg	
180 185 190	
Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile	
195 200 205	
Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser	

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Tyr Gln Leu Ser Leu Glu	Tyr Gln Leu His Pro Ser His Gln Ile Ala	
225 230	235	240
Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr		
245	250	255
Phe Glu Asp Arg Gly Lys Ser Ser Gln Phe Leu Pro Asn Pro Asp		
260	265	270
Leu Gln Pro Glu Thr Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln		
275	280	285
Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His		
290 295	300	
Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu		
305 310	315	320
Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe		
325	330	335
Val Asn Glu Pro Glu Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala		
340	345	350
Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu		
355	360	365
Lys Gly Ser Tyr Ser Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys		
370	375	380
Ser Ile Gln Pro Trp Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu		
385 390	395	400
Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala		
405	410	415
Lys Asp Ala Ile Glu Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys		
420	425	430
Gln Trp Pro His Leu Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly		
435	440	445
Gln Val		
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aacaacccac cccgtagggc acggctgttt cttttgaga aattacgctt cttcatcttg 240
atctttttc aagatctcat cttcattgag ttttaaaaga cgggcaatcg cattgcggta 300
ggagatttca aggcttctc gactagtgc aatgacacact tgatcgatta agaaaccgtc 360
attgacatca taaacccaac catgtaatga gagtttttc ccattttcc acgcggattt 420
aatgattgac gagcgaccta agttataaac ttgctctgcg acgttaattt tcgtcagcat 480
atcagcccggt tttcaggcg gtaaattgcc aagtaaatga ctatgcttat accaaatatc 540
gcgttaagtgg agtaaccagt tattaattaa acctaaatct tgatccgcca ttgcggcttt 600
aattccacca cagtttgtat gtccacaaat aataatgtgt tcaatattta agacctcaac 660
ggcatattgc acaacagata aacagttaa atcgggtgtga atgacttgat ttgcaacatt 720
acgatgcaca aacagctcac ccggcctaa atttgttaat tttctgcag gaacacggct 780
atccgagcaa ccaatccaaa gatagctcg ggttgatga tcagccaatt cttaaagta 840
agaggagttt tcctctttca tccgtAACgc ccagctataa ttattggcaa aaagttgttc 900
aattttttc attagagtga ttccataacc gcaaaaataa gggggctagt atagcttaga 960
aatagacagt gggtaaagaa aggcaaaaaa ttgtatagga taacttgttt ttatattgcca 1020
tttatttaga attagaatct ttaataataa aaataattat cattaaggaa aatagtt 1077
atg gat aaa aat tta atg aag gga tgt gta ttc tta tca ata gtc ggt 1125
Met Asp Lys Asn Leu Met Lys Gly Cys Val Phe Leu Ser Ile Val Gly
1 5 10 15
tgc ggt atc caa ata ggg cta gca tca aat cca aat cct cca gat gtg 1173
Cys Gly Ile Gln Ile Gly Leu Ala Ser Asn Pro Asn Pro Pro Asp Val
20 25 30
gat gag tta tta cct att att gtg aat gct gat gaa gat aat aaa tta 1221
Asp Glu Leu Leu Pro Ile Ile Val Asn Ala Asp Glu Asp Asn Lys Leu
35 40 45
cca ggt cgt tct gta tta aaa cag aaa aat atc gat caa caa caa gca 1269
Pro Gly Arg Ser Val Leu Lys Gln Lys Asn Ile Asp Gln Gln Gln Ala
50 55 60
gat aat gcc gct gac tta ata aat att tta cct ggg gta aat atg gcg 1317
Asp Asn Ala Ala Asp Leu Ile Asn Ile Leu Pro Gly Val Asn Met Ala
65 70 75 80
gga gga ttt cgc cct ggt ggt caa aca tta aat att aat gga atg ggt 1365
Gly Gly Phe Arg Pro Gly Gly Gln Thr Leu Asn Ile Asn Gly Met Gly
85 90 95
gat gct gaa gat gtt aga gtt caa cta gac ggc gca aca aaa agt ttc 1413
Asp Ala Glu Asp Val Arg Val Gln Leu Asp Gly Ala Thr Lys Ser Phe
100 105 110
gaa aaa tat caa caa ggc tct att ttt att gaa cct gag tta tta aga 1461

Glu	Lys	Tyr	Gln	Gln	Gly	Ser	Ile	Phe	Ile	Glu	Pro	Glu	Leu	Leu	Arg	
115							120						125			
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Lys	Val	Thr	Val	Asp	Lys	Gly	Asn	Tyr	Ser	Pro	Gln	Tyr	Gly	Asn	Gly	
130							135					140				
ggc	ttt	gct	ggt	act	gta	aaa	ttt	gaa	aca	aaa	gat	gca	act	gat	ttt	1557
Gly	Phe	Ala	Gly	Thr	Val	Lys	Phe	Glu	Thr	Lys	Asp	Ala	Thr	Asp	Phe	
145							150				155				160	
ttg	aaa	gaa	aat	cag	aaa	ata	ggt	gga	tta	ttt	aaa	tat	gga	aat	aat	1605
Leu	Lys	Glu	Asn	Gln	Lys	Ile	Gly	Gly	Leu	Phe	Lys	Tyr	Gly	Asn	Asn	
165							170					175				
agc	aat	aat	aac	caa	aaa	act	tat	agt	aca	gcc	cta	gtt	tta	cag	aat	1653
Ser	Asn	Asn	Asn	Gln	Lys	Thr	Tyr	Ser	Thr	Ala	Leu	Val	Leu	Gln	Asn	
180							185					190				
gaa	caa	aaa	aat	att	gat	ttg	tta	tta	ttt	ggt	tct	gta	aga	aat	gca	1701
Glu	Gln	Lys	Asn	Ile	Asp	Leu	Leu	Leu	Phe	Gly	Ser	Val	Arg	Asn	Ala	
195							200					205				
agc	aat	tat	aca	aga	cct	gat	aaa	agt	aaa	att	ctt	ttt	tca	aaa	aac	1749
Ser	Asn	Tyr	Thr	Arg	Pro	Asp	Lys	Ser	Lys	Ile	Leu	Phe	Ser	Lys	Asn	
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aat	caa	aaa	agt	gga	tta	ata	aaa	gta	aat	tgg	caa	att	act	cct	gaa	1797
Asn	Gln	Lys	Ser	Gly	Leu	Ile	Lys	Val	Asn	Trp	Gln	Ile	Thr	Pro	Glu	
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His	Leu	Leu	Thr	Leu	Ser	Ser	Val	Tyr	Gly	Ile	His	Lys	Gly	Trp	Glu	
245							250					255				
cct	tgg	gca	gca	aaa	aga	gat	gtg	atg	tcg	aga	cca	aca	gaa	aca	gaa	1893
Pro	Trp	Ala	Ala	Lys	Arg	Asp	Val	Met	Ser	Arg	Pro	Thr	Glu	Thr	Glu	
260							265					270				
ata	aaa	cac	tat	ggg	att	gat	gtt	gcg	tgg	aaa	cgt	aaa	ctt	gtt	tat	1941
Ile	Lys	His	Tyr	Gly	Ile	Asp	Val	Ala	Trp	Lys	Arg	Lys	Leu	Val	Tyr	
275							280					285				
cga	gat	caa	aaa	gat	gaa	agt	tat	tca	ttg	aaa	tat	cgc	tat	tta	cct	1989
Arg	Asp	Gln	Lys	Asp	Glu	Ser	Tyr	Ser	Leu	Lys	Tyr	Arg	Tyr	Leu	Pro	
290							295					300				
gaa	aat	aat	aag	tgg	att	aat	ttg	tct	gtt	cag	ctg	agt	tat	agt	aaa	2037
Glu	Asn	Asn	Lys	Trp	Ile	Asn	Leu	Ser	Val	Gln	Leu	Ser	Tyr	Ser	Lys	
305							310				315				320	
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Thr	Glu	Gln	Asn	Asp	Thr	Arg	His	Glu	Lys	Val	Thr	Ser	Ser	Phe	Leu	
325							330					335				
ggt	aca	tta	gga	aat	aaa	agt	tgg	ata	act	tat	tca	gat	ctt	act	ttt	2133
Gly	Thr	Leu	Gly	Asn	Lys	Ser	Trp	Ile	Thr	Tyr	Ser	Asp	Leu	Thr	Phe	
340							345					350				
gat	ata	agt	aac	aca	agt	act	cta	aat	att	ggg	cgt	gct	gag	cat	gaa	2181
Asp	Ile	Ser	Asn	Thr	Ser	Thr	Leu	Asn	Ile	Gly	Arg	Ala	Glu	His	Glu	
355							360					365				

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aaagaccacc acggcgtcg tggttattg cgtatggtt ctcgtcgtcg taaacttta 8032

gattactaa aacgtactaa tcttgagctt tacacttcaa ctatcgctcg tttaggttt 8092

cgtcgctaat ttgttatttcc aacaaaaaac cttgataat ttatcaagg 8152

gttttctttt ttctgcatac taggcatgtt taaattatcg caaaacacac cgacatttc 8212

gtggaaaagt gcggcattt tttaattta ttacttct taaaacatga tctcacttgg 8272

gattactgaa cttgcccagt aaagctcagt agcgactttt tcagctaatt gcataaacga 8332

ttgggcaatg tcgctttcag gtgcggcgc aacggttggg ataccttgc taaatcttc 8392

acgtaaacgaa atatgtaatg cctgttgcc taaaactttt acattatatt ttgtgcaat 8452

gcgctcagca ccgcctgttc cggaaatcgt ttcttgc tccacaattgc tacaatatg 8512

catcgacata tttcgataa tgcctaaaac gggtagacaa acacgctcaa acatcgccac 8572

acctttaatc gcatccagta aagcaatatc ttgtgggtt gtcaccacga cggccccgt 8632

cactggaaatt tggtgagaaa gggcagctg gatatcccgt gtacccggc gcatatcaat 8692

gactaaataa tctaaatcag gccataaggt ttcttgc taaaactttt acattatatt ttgtgcaat 8752

tgcatttgc cgcgcacaa tcgtgcatt gtccggccat taaaatgc aatggaaatt 8812

ggcaaaaata tgatgtgctt gaattgggtt aatgtgctgg ttatctggc aagttggc 8872

ttgatcagca acccctaaca tgcgtggaaat agatggacca taaaatgcg catctaaaat 8932

tccaaacacga gcacccttgc tttgtaaaggc aagagcaaga ttgacggaaa tagtagattt 8992

tcctacacca ctttaccccg atgtcagcc aataatattt tttacccctt ttacggctgg 9052

gtggcttata gcgcgtttt aatgtcgat ttgataattt aattggcatt tgatgtcttt 9112

gcattctgct aatgtgagaa gttctgtgga gagagcgctc ttgagttgtt cgaatgcagt 9172
attccaagca aacggcatgc tgatttcaat acgtaacgtc tcaccgcctt tttcaatttt 9232
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tgtgtttgg atagcttgtt ttgactgtc cgttaaactg tcagaaaata aaattcccat 9352
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aattcatttta gggcatttat tagaacatat tcaagcagat atttgggtgc gttccaacgt 9652
atgcgtgggc ataaagtgc a tttatttgtt gcagatgtg cccatggcac accaatcatg 9712
ttaaatgcga taaatttaggt attacaccaa agcattaatt gtcctcgaa agcagaacat 9772
gtggcggatt tgaaggctta atattagcta tgataatatc at 9814

<210> 32

<211> 967

<212> PRT

<213> *Pasteurella multocida*

<400> 32

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Ser Tyr Cys Gly Thr Ile Leu Ala Asp Ser His Gln Glu Ala Thr Glu
20 25 30

Leu Asp Thr Ile Thr Val Ser Ser Gln Gln Asp Glu Met Asn Ile Lys
35 40 45

Glu Lys Lys Ile Gly Glu Thr Val Lys Thr Ala Ser Gln Leu Lys Arg
50 55 60

Gln Gln Val Gln Asp Ser Arg Asp Leu Val Arg Tyr Glu Thr Gly Val
65 70 75 80

Thr Val Val Glu Ala Gly Arg Phe Gly Ser Ser Gly Tyr Ala Ile Arg
85 90 95

Gly Val Asp Glu Asn Arg Val Ala Ile Thr Val Asp Gly Leu His Gln
100 105 110

Ala Glu Thr Leu Ser Ser Gln Gly Phe Lys Glu Leu Phe Glu Gly Tyr
115 120 125

Gly Asn Phe Asn Asn Thr Arg Asn Ser Val Glu Ile Glu Thr Leu Lys
130 135 140

Val Ala Lys Ile Ala Lys Gly Ala Asp Ser Val Lys Val Gly Ser Gly
145 150 155 160

Ser Leu Gly Gly Ala Val Leu Phe Glu Thr Lys Asp Ala Arg Asp Phe
165 170 175

Leu Thr Glu Lys Asp Trp His Ile Gly Tyr Lys Ala Gly Tyr Ser Thr
180 185 190

Ala Asp Asn Gln Gly Leu Asn Ala Val Thr Leu Ala Gly Arg Tyr Gln
195 200 205

Met Phe Asp Ala Leu Ile Met His Ser Lys Arg His Gly His Glu Leu
210 215 220

Glu Asn Tyr Asp Tyr Lys Asn Gly Arg Asp Ile Gln Gly Lys Glu Arg
225 230 235 240

Glu Lys Ala Asp Pro Tyr Thr Ile Thr Lys Glu Ser Thr Leu Val Lys
245 250 255

Phe Ser Phe Ser Pro Thr Glu Asn His Arg Phe Thr Val Ala Ser Asp
260 265 270

Thr Tyr Leu Gln His Ser Arg Gly His Asp Leu Ser Tyr Asn Leu Val
275 280 285

Ala Thr Thr His Ile Gln Leu Asp Glu Lys Glu Ser Arg His Ala Asn
290 295 300

Asp Leu Thr Lys Arg Lys Asn Val Ser Phe Thr Tyr Glu Asn Tyr Thr
305 310 315 320

Val Thr Pro Phe Trp Asp Thr Leu Lys Leu Ser Tyr Ser Gln Gln Arg
325 330 335

Ile Thr Thr Arg Ala Arg Thr Glu Asp Tyr Cys Asp Gly Asn Glu Leu
340 345 350

Cys Asp Ser Tyr Lys Asn Pro Leu Gly Leu Gln Phe Lys Asp Gly Gln
355 360 365

Ile Leu Asp Pro Ala Gly Asn Lys Ile Lys Leu Gln Gly Ser Gly Leu
370 375 380

Ser Thr Gln Ile Val Asp Glu Asn Gly Lys Pro Phe Pro Thr Thr Thr
385 390 395 400

Gly Thr Asn Asn Ala Ala Phe Ser Asn Asn Leu Arg Leu Arg Pro Thr
405 410 415

Gly Phe Trp Leu Asp Cys Ser Val Phe Asp Cys Asn Lys Pro Phe Thr
420 425 430

Val Tyr Asn Ile Ser Asn Gly Thr Tyr Gln Ala Arg Glu Val Leu Leu
435 440 445

Ser Glu Glu Ile Thr Val Asp Gly Lys Leu Tyr Lys Thr Ala Lys Glu
450 455 460

Glu Gly Gly Leu Pro Asn Tyr Leu Ile Leu Pro Asn Ser Lys Gly Tyr
465 470 475 480

Leu Pro Tyr Asp Tyr Lys Glu Arg Asp Leu Asn Thr Asn Thr Lys Gln
485 490 495

Ile Asn Leu Asp Leu Thr Lys Thr Phe Leu Thr Phe Asn Ile Glu Asn
500 505 510

Asn Leu Ser Tyr Gly Gly Val Tyr Ser Arg Ile Glu Lys Glu Met Ile
515 520 525

Asn Lys Ala Gly Tyr Glu Gly Arg Asn Pro Thr Trp Trp Ala Asp Arg
530 535 540

Ile Leu Gly Gln Ser Ser Tyr Cys Gly Tyr Asn Ala Leu Lys Cys Pro
545 550 555 560

Lys His Glu Pro Leu Thr Ser Phe Leu Ile Pro Val Glu Ala Thr Thr
565 570 575

Gln Ser Leu Tyr Phe Ala Asn Ile Leu Lys Val His Asn Met Ile Ser
580 585 590

Ile Asp Leu Gly Tyr Arg Tyr Asp His Ile Lys Tyr Asn Pro Glu Tyr
595 600 605

Thr Pro Gly Val Thr Pro Lys Ile Pro Asp Asp Met Val Lys Gly Leu
610 615 620

Phe Ile Pro Met Pro Lys Glu Pro Gln Leu Lys Asp Phe Asp Tyr Asn
625 630 635 640

Tyr Ala Lys Phe Gly Glu Ala Tyr Lys Lys Trp Lys Glu Tyr Leu Pro
645 650 655

Lys Asn Ala Glu Glu Asn Ile Ala Tyr Ile Ala Gln Asp Lys Thr Phe
660 665 670

Lys Lys His Ser Tyr Ser Leu Gly Ala Thr Phe Asp Pro Leu Asn Phe
675 680 685

Leu Arg Val Gln Val Lys Tyr Ser Lys Gly Phe Arg Ala Pro Thr Ser
690 695 700

Asp Glu Leu Tyr Phe Thr Phe Lys His Pro Asp Phe Thr Ile Leu Pro
705 710 715 720

Asn Pro Val Leu Lys Pro Glu Glu Ala Lys Asn Gln Glu Ile Ala Leu
725 730 735

Thr Val His Asp Asn Trp Gly Phe Val Ser Thr Ser Val Phe Gln Thr
740 745 750

Lys Tyr Arg His Phe Ile Asp Leu Ala Tyr Leu Gly Ser Arg Asn Leu
755 760 765

Ser Asn Ser Val Gly Gly Gln Ala Gln Ala Arg Asp Phe Gln Val Tyr
770 775 780

Gln Asn Val Asn Val Asp Asn Ala Lys Val Lys Gly Leu Glu Ile Asn
785 790 795 800

Ala Arg Leu Asn Leu Gly Tyr Phe Trp His Val Leu Asp Gly Phe Asn
805 810 815

Thr Ser Tyr Lys Phe Thr Tyr Gln Arg Gly Arg Leu Asp Gly Asp Arg
820 825 830

Pro Met Asn Ala Ile Gln Pro Lys Ala Ser Val Phe Gly Leu Gly Tyr
835 840 845

Asp His Lys Glu Asn Lys Phe Gly Ala Asp Leu Tyr Ile Thr Arg Val
850 855 860

Ser Glu Lys Lys Ala Lys Asp Thr Tyr Asn Met Phe Tyr Lys Glu Gln
865 870 875 880

Gly Tyr Lys Asp Ser Ala Val Arg Trp Arg Ser Asp Asp Tyr Thr Leu
885 890 895

Val Asp Ala Val Gly Tyr Ile Lys Pro Ile Lys Asn Leu Thr Leu Gln
900 905 910

Phe Gly Val Tyr Asn Leu Thr Asp Arg Lys Tyr Leu Thr Trp Glu Ser
915 920 925

Ala Arg Ser Ile Lys Pro Phe Gly Thr Ser Asn Leu Ile Asn Gln Lys
930 935 940

Thr Gly Ala Gly Ile Asn Arg Phe Tyr Ser Pro Gly Arg Asn Phe Lys
945 950 955 960

Leu Ser Ala Glu Ile Thr Phe
965

<210> 33

<211> 2990

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (1106)..(1564)

<220>

<223> kdtB

<400> 33

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tggtgccgca accgcgccag ggactttgtt ataaaacggtt tgataacggtt ctttatccgc 120

ttcttcgtca gggcgatcaa tataaggggg caatggcata tgcccaattt gctgtaacac 180

gtctaaaagt gcggctgtt tttgcgcgtt ttcttaattca aataaggtat catggcgcgc 240

aaccatgatc attttgacac catgatgttc acctaactta tcttcgccta accacagttc 300

tgccccttct ttcggtgctt ttgaggagcg cacatggct aaaaagcgtg tgtcgatata 360

aatccgctcg accaacactt ccaccttacc gccactggct ttacgtccaa acatccttgc 420

aggaatcacg cgctgttat taaaaattaa taagtcgcct tcatgaattt gatcaaggat 480

atcagcaaaa gtgcgggtgg taatctcacc atttcgccg ttaagttgttataaagcgact 540

agcgggtgcga tccgggttttggtaacgagc aatcagctca tcgggtaaat caaaataaaaa 600

gtcagaaaaca cgcataaaata gggttataaa aagttatcta aaaaatcgtg ggcgtaaatc 660

tagtgtgaat tccgcttttgc cacaaggaaa aatccagatt ttgttgttta gtatcgaatt 720

gagatgattt tggacaaaaaaa aaaagccctt tcaagaaaaga cggaaagggcg aaaatataattt 780

tgaggatcata ctttttaggg tatgtgtcgg attatacaca caaaaataac aatgcaaca 840
tttttttaac aatcatatgt aagcgtattg tgtgagaacg agcgtaaaaa tgaacgcatt 900
ctaaaggatg atttatttag cctattaaa aaacacatga gatgagagtt tgcgagagcg 960
gtaataaaaag tgcggtgggt ttttagaaaag ttttgaatag gatcacaaat taaacaaaagt 1020
ttgtgaaata ccaagtagta gtttttaagt atatgatgaa tcatatgcta aagtttaaac 1080
ccgttaata accaagaggt ggaag atg aca gaa gaa aat aaa gga aag aga 1132
Met Thr Glu Glu Asn Lys Gly Lys Arg
1 5
tat ttt tta tgg ttc ata ttg ttt atc ctt tca atc tat tta ttt att 1180
Tyr Phe Leu Trp Phe Ile Leu Phe Ile Leu Ser Ile Tyr Leu Phe Ile
10 15 20 25
acc ata caa gaa aga cga ggt tat tgt ttt gac aaa cgt gca tat att 1228
Thr Ile Gln Glu Arg Arg Gly Tyr Cys Phe Asp Lys Arg Ala Tyr Ile
30 35 40
cat gag ctt tat act gag caa gag tta att gat cgg ggg att gaa tat 1276
His Glu Leu Tyr Thr Glu Gln Glu Leu Ile Asp Arg Gly Ile Glu Tyr
45 50 55
gtg gta tcc acc atg ccg tca ggt gtt att aaa cca gat ggc aca ata 1324
Val Val Ser Thr Met Pro Ser Gly Val Ile Lys Pro Asp Gly Thr Ile
60 65 70
aaa gaa gta aag cgt tac acg agt gtc gag gag ttt aaa cag atg aac 1372
Lys Glu Val Lys Arg Tyr Thr Ser Val Glu Glu Phe Lys Gln Met Asn
75 80 85
cca gct tgt tgt aca tta acc acc ttt att gat gaa gga ggc gat ggc 1420
Pro Ala Cys Cys Thr Leu Thr Thr Phe Ile Asp Glu Gly Gly Asp Gly
90 95 100 105
tat cca gat gat gat gga tat ggt tat gtc aga att gaa tat tta aga 1468
Tyr Pro Asp Asp Asp Gly Tyr Gly Tyr Val Arg Ile Glu Tyr Leu Arg
110 115 120
cat tat gtt gag aat cta aaa cct tat cat aga gtg att tat ctt gaa 1516
His Tyr Val Glu Asn Leu Lys Pro Tyr His Arg Val Ile Tyr Leu Glu
125 130 135
tat acg ccc tgt gga gag tta agg gaa gag gcg gct ttt tca aaa aat 1564
Tyr Thr Pro Cys Gly Glu Leu Arg Glu Glu Ala Ala Phe Ser Lys Asn
140 145 150
taagagttagt gtaagaaaat ggcattacca acagcaacaa taatgaggaa tttatcttta 1624
tctaaaaatc aattcactct gaaagggatg gaatgcgtag attccctatt tcaagcatgc 1684
agtaatatgg atcatggta ctgaggtgga agatggcaga agaaaataaa ggaaagagat 1744
atttttatg gttcatattg tttatcctt caatctattt atttattacc atacaagaaa 1804
gacgaggtta ttgtttgac aaatggaaat atatccataa cctttataacc gagcaagagt 1864
tgatcgatag aggggttgaa tatgtggat ccaccatgcc gtcaggtgtt tttgaaccag 1924
atggcacaac aaccgaaata aaacgtttagt ctatgttga ggagttaaa cagatgaacc 1984

ctgattgttg taaattaaca agatttatta atgaaggaat agatggctat ccagatgatg 2044
atggatatgg ttatataaga attgaatatt taagacatta tggtggaaat tttaaacctg 2104
atcatagagt gcttatctc gaatatacgc cttgtggaga attaaggaa gaggtttctt 2164
tttaaaaaat aaataatagt gaggtgaaga aatggcatta ccaacagcaa cagaaatcac 2224
aaatgcatac ttatataaaa ataaattaac tcctaaagcg gaggaaagag tagattcaat 2284
acaaattctt gaaaaaggag atgaacattt cgaagtaat tttaattgat caaagtactc 2344
tattgattga aggaaaaaca gtgaaattaa tggcaggat ggcagttct gcggaaatta 2404
aaacaggtaa acgcagtgtt ttagattact tatttagccc attaaaaacc acaaataat 2464
attaaggaga ataatatgtc gtataataa tatactgtt ctttGattac gttctcaaca 2524
gggatctgtt ttccggcaat atgctacgct ctaaattcgc tggatatacg atcctgttt 2584
agactatgtt gaaaagacta aactttgtt ggttaactgg gttcggtaa aattctggaa 2644
acaaatgggc ttaacccgcg tgatcttac ccgtgagctt tcgcttgatg aaattgccc 2704
aattcgtcag caagtgcag aaatggaaat tgaagtgtt gtcgtggg cattatgc 2764
ggcgtattct ggacgttgg tattatcagg ctatattaat aaacgtgatc caaatcaagg 2824
cacctgtacc aatgcgtgcc gttggaaata cagtgtacc gaagccaaag aagatgagat 2884
cgccaacatt gtgaatgtgg gtgaagaaat tccagtgaaa aatgtagcac cgacacttgg 2944
cgaaggcgac accaccagta aagtattttt attagcagaa agtcga 2990

<210> 34
<211> 153
<212> PRT
<213> Pasteurella multocida

<400> 34
Met Thr Glu Glu Asn Lys Gly Lys Arg Tyr Phe Leu Trp Phe Ile Leu
1 5 10 15
Phe Ile Leu Ser Ile Tyr Leu Phe Ile Thr Ile Gln Glu Arg Arg Gly
20 25 30
Tyr Cys Phe Asp Lys Arg Ala Tyr Ile His Glu Leu Tyr Thr Glu Gln
35 40 45
Glu Leu Ile Asp Arg Gly Ile Glu Tyr Val Val Ser Thr Met Pro Ser
50 55 60
Gly Val Ile Lys Pro Asp Gly Thr Ile Lys Glu Val Lys Arg Tyr Thr
65 70 75 80
Ser Val Glu Glu Phe Lys Gln Met Asn Pro Ala Cys Cys Thr Leu Thr
85 90 95
Thr Phe Ile Asp Glu Gly Gly Asp Gly Tyr Pro Asp Asp Asp Gly Tyr
100 105 110
Gly Tyr Val Arg Ile Glu Tyr Leu Arg His Tyr Val Glu Asn Leu Lys

115 120 125

Pro Tyr His Arg Val Ile Tyr Leu Glu Tyr Thr Pro Cys Gly Glu Leu
130 135 140

Arg Glu Glu Ala Ala Phe Ser Lys Asn
145 150

<210> 35
<211> 1683
<212> DNA
<213> *Pasteurella multocida*

<220>
<221> CDS
<222> (325)..(1230)

<220>
<223> lgtC

<220>
<223> Nucleotides at positions 981, 1000, 1129, 1134,
and 1144 are A, T, C or G. The corresponding
amino acids are unknown.

<400> 35
atataaagt ctcatggcaa gaaaattaga aaagagcgat caattattat ttgcaagatt 60
tgggtattat tcataaggcta ggtgaaagat atattttcc atgatattaa aacgattcag 120
gcagaactgg ctagcttatac acttttagat aattgttatta ttaaaagaag ctgtatgatt 180
gttattctat cattagtggta taataaatat tctttatttt ttgagagata aaaacaattc 240
atatttcaat agaaaacaga aaataaagat tatcaaaaga attatccgtc cttataaata 300
tgagtctgtat ttgtgagatg atat atg aat att tta ttt gtt tct gat gat 351
Met Asn Ile Leu Phe Val Ser Asp Asp
1 5

gtt tat gct aaa cat ctg gtg gtc att aaa agc att ata aat cat 399
Val Tyr Ala Lys His Leu Val Val Ala Ile Lys Ser Ile Ile Asn His
10 15 20 25

aat gaa aaa ggt att tca ttt tat att ttt gat ttg ggt ata aag gat 447
Asn Glu Lys Gly Ile Ser Phe Tyr Ile Phe Asp Leu Gly Ile Lys Asp
30 35 40

gaa aat aag aga aat att aat gat att gtt tct tct tat gga agt gaa 495
Glu Asn Lys Arg Asn Ile Asn Asp Ile Val Ser Ser Tyr Gly Ser Glu
45 50 55

gtc aac ttt att gct gtg aat gag aaa gaa ttt gag agt ttt cct gtt 543
Val Asn Phe Ile Ala Val Asn Glu Lys Glu Phe Glu Ser Phe Pro Val
60 65 70

caa att agt tat att tct tta gca aca tat gca agg cta aaa gcg gca 591
Gln Ile Ser Tyr Ile Ser Leu Ala Thr Tyr Ala Arg Leu Lys Ala Ala
75 80 85

gag tat ttg ccg gat aat tta aat aaa att att tat tta gat gtt gat 639
Glu Tyr Leu Pro Asp Asn Leu Asn Lys Ile Ile Tyr Leu Asp Val Asp

90	95	100	105	
gtt ttg gtt ttt aac tca tta gaa atg tta tgg aat gtt gat gtt aat				687
Val Leu Val Phe Asn Ser Leu Glu Met Leu Trp Asn Val Asp Val Asn				
110		115	120	
aat ttt ctt acc gca gcc tgt tat gat tct ttc atc gaa aat gaa aag				735
Asn Phe Leu Thr Ala Ala Cys Tyr Asp Ser Phe Ile Glu Asn Glu Lys				
125		130	135	
tct gag cat aaa aaa tcg att tca atg tca gat aag gaa tat tat ttt				783
Ser Glu His Lys Lys Ser Ile Ser Met Ser Asp Lys Glu Tyr Tyr Phe				
140		145	150	
aat gca gga gta atg cta ttt aat tta gat gaa tgg cgg aag atg gat				831
Asn Ala Gly Val Met Leu Phe Asn Leu Asp Glu Trp Arg Lys Met Asp				
155		160	165	
gta ttc tca aga gct tta gac ctg tta gct atg tat cct aat caa atg				879
Val Phe Ser Arg Ala Leu Asp Leu Leu Ala Met Tyr Pro Asn Gln Met				
170		175	180	185
att tat cag gat caa gat ata ttg aat atc ctt ttt agg aat aaa gtc				927
Ile Tyr Gln Asp Gln Asp Ile Leu Asn Ile Leu Phe Arg Asn Lys Val				
190		195	200	
tgt tat tta gat tgc aga ttt aat ttc atg cca aat caa ctt gaa aga				975
Cys Tyr Leu Asp Cys Arg Phe Asn Phe Met Pro Asn Gln Leu Glu Arg				
205		210	215	
ata aan caa tac cat aaa gga aaa ntg agc' aac tta cat tct tta gaa				1023
Ile Xaa Gln Tyr His Lys Gly Lys Xaa Ser Asn Leu His Ser Leu Glu				
220		225	230	
aaa aca acg atg cct gtc gtt att tca cat tat tgt ggt cca gaa aaa				1071
Lys Thr Thr Met Pro Val Val Ile Ser His Tyr Cys Gly Pro Glu Lys				
235		240	245	
gcg tgg cat gcg gat tgt aaa cat ttt aat gta tat ttc tat cag aaa				1119
Ala Trp His Ala Asp Cys Lys His Phe Asn Val Tyr Phe Tyr Gln Lys				
250		255	260	265
ata tta gca naa atn tcg aga ggc ncg gat aaa gaa cgc gta tta tct				1167
Ile Leu Ala Xaa Xaa Ser Arg Gly Xaa Asp Lys Glu Arg Val Leu Ser				
270		275	280	
ata aaa act tat ctc aag gcc ttg att aga agg att aga tat aaa ttc				1215
Ile Lys Thr Tyr Leu Lys Ala Leu Ile Arg Arg Ile Arg Tyr Lys Phe				
285		290	295	
aaa tat caa gtc tat taactattga attttgcaa atgagataag agtatagtgc				1270
Lys Tyr Gln Val Tyr				
300				
tgatttcttc aaagcgaaaa ggaggaaata gcttgttcta atttattaca ataatggttg				1330
tattcatctt gatttgaaag gaaagagagt gtttttgcata taaaagcatt ttcgtcacct				1390
aaatttacta atcctccaaa ttctcctcct cgnagaattt ctttggacc gtagggcag				1450
tccatggata ttacaggtgt accgcaagcc atgctttcta ggataactgt cggtaacccc				1510
tctttcaaag aggtgtgtaa aaatagctta gcattttta ttaatggata cggattatct				1570

ttatcccta aaagaaaaca atcttcttgt agattgagtg attctatgg tttctcta 1630
tttctcgac actcaccatc ccaaacaata tatancntt cttggatacc tcc 1683

<210> 36
<211> 302
<212> PRT
<213> Pasteurella multocida

<400> 36
Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
1 5 10 15
Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
20 25 30
Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
35 40 45
Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
50 55 60
Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
65 70 75 80
Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
85 90 95
Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
100 105 110
Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
115 120 125
Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
130 135 140
Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
145 150 155 160
Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp
165 170 175
Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile
180 185 190
Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
195 200 205
Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Xaa Gln Tyr His Lys Gly
210 215 220
Lys Xaa Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
225 230 235 240
Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
245 250 255
His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Xaa Xaa Ser Arg
260 265 270
Gly Xaa Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala

275 280 285

Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr
290 295 300

<210> 37
<211> 2029
<212> DNA
<213> *Pasteurella multocida*

<220>
<221> CDS
<222> (2)..(499)

<220>
<223> *mglB*

<220>
<223> Nucleotides at positions 98, 296 and 302 are A, T, G, or C. The corresponding amino acids are unknown.

<220>
<223> Nucleotides at positions 928, 1007, 1740, 1808, 1816, and 1820 are A, T, G, or C.

<400> 37

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	Leu	Asn	Lys	Ala	Gly	Lys	Ile	Gln	Tyr	Val	Leu	Leu	Lys	Gly	Asn	Gln	15
1				5						10							

gga cac cca gat gca gaa gct cgt aca aaa ttc gtc att aaa gaa tta 97
Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
20 25 30

nat aat aaa ggc att caa gat gag caa tta ttc atc gac acg ggg atg 145
Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
35 40 45

tgg gat gcc gct tta gcg aaa gat aaa atg gat gca tgg tta tct agc 193
Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
50 55 60

tct aaa gca aat caa att gaa gtg atc atc gct aac aac gat ggt atg 241
Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
65 70 75 80

gcg atg ggg gca ttg gaa gcc acg aaa gca cat ggt aaa aaa tta cca 289
Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
85 90 95

atc ttc ngt gta nat gcg tta cca gaa gtc ctc caa tta atc aaa aaa 337
Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
100 105 110

ggt gaa att gca ggt acg gtg tta aat gac ggt gtg aac caa ggt aaa 385
Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
115 120 125

gcc gtt gtt caa tta agt aat aat ctt gca aaa gga aaa cct gcc act 433
Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
130 135 140

gaa ggc aca aaa tgg cag tta aaa cga tcg tgt cct acg tat ccc tta 481
Glu Gly Thr Lys Trp Gln Leu Lys Arg Ser Cys Pro Thr Tyr Pro Leu
145 150 155 160

tgt tgg tgt gga tgc gga taacttaaac gagttcctaa aataataaac 529
Cys Trp Cys Gly Cys Gly
165

tataacaaaa caagamgtt gtaattctcg ggaggtatac cctcccccctt tttatgtgag 589
gttggatatg acaactcaa ttccaaatca agacagtgaa atactgctca caatgaccaa 649
cgtctgtaaa tcctttcccg gtgttaaagc gttagacaat gcaaacctaa ctgtgcgc 709
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aaacgccatc acaaaaccna tattggntca ntatctgggg tggtaaccaa caaaaagtgg 1849
tcattggtcg ttgggttatta acccaccctg aaatcttgcgtt gtttagacgaa ccaacacgtg 1909
gtatcgacat tgggtgcgaaa tatgaaattt atcagctgat tatggagttt gccaaaaaag 1969
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<210> 38
<211> 166
<212> PRT
<213> Pasteurella multocida

<400> 38
Leu Asn Lys Ala Gly Lys Ile Gln Tyr Val Leu Leu Lys Gly Asn Gln
1 5 10 15
Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
20 25 30
Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
35 40 45
Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
50 55 60
Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
65 70 75 80
Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
85 90 95
Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
100 105 110
Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
115 120 125
Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
130 135 140
Glu Gly Thr Lys Trp Gln Leu Lys Arg Ser Cys Pro Thr Tyr Pro Leu
145 150 155 160
Cys Trp Cys Gly Cys Gly
165

<210> 39
<211> 2628
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (326) .. (766)

<220>
<223> mioC

<400> 39
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agaaaattta gatcagttag aagaaaaat taaacaagcg gttgaaacta tccaaattact 120
tcaattggaa attgatgaat taaaagaaaa aaataaccaa tctcaacaag caaatgacgc 180
attacgcagt gaaaatgaac aactaaagag tgagcaccaa aactggcaag aacgtttacg 240
ctcatttatta ggcaaaattt gataacgtata attcacttct tattaaggct tagttttct 300
aaggcatttattt ttttaggaga aatta atg aaa aca aaa att tgt att atc act 352
Met Lys Thr Lys Ile Cys Ile Ile Thr
1 5

ggc agt acg ctt ggt gca gaa tat gtt gca gaa cat att gct gaa 400

Gly Ser Thr Leu Gly Gly Ala Glu Tyr Val Ala Glu His Ile Ala Glu
10 15 20 25

ata tta gaa caa caa gat tat cct gta cgt tta gaa cat gga cca aat 448
Ile Leu Glu Gln Gln Asp Tyr Pro Val Arg Leu Glu His Gly Pro Asn
30 35 40

ttt gaa gaa gtg atc gat gaa aaa tgt tgg ctt gtt gtc acc tct acc 496
Phe Glu Glu Val Ile Asp Glu Lys Cys Trp Leu Val Val Thr Ser Thr
45 50 55

cat ggt gca ggt gaa tta ccg gat aat att aaa cct ctg ttt gaa aaa 544
His Gly Ala Gly Glu Leu Pro Asp Asn Ile Lys Pro Leu Phe Glu Lys
60 65 70

tta gca ttt cac cca aaa cag tta gct gac tta cgc ttt gcg gtg atc 592
Leu Ala Phe His Pro Lys Gln Leu Ala Asp Leu Arg Phe Ala Val Ile
75 80 85

ggg tta ggt aat tcg gat tat gat acc ttc tgt cac gca gtg gat cat 640
Gly Leu Gly Asn Ser Asp Tyr Asp Thr Phe Cys His Ala Val Asp His
90 95 100 105

gtg gaa caa tta ctg cta agc aaa gat gct tta caa ctg tgt gaa tcg 688
Val Glu Gln Leu Leu Ser Lys Asp Ala Leu Gln Leu Cys Glu Ser
110 115 120

cta aga atg gat atg cta acc att act gat cct gaa cac acg gcc gaa 736
Leu Arg Met Asp Met Leu Thr Ile Thr Asp Pro Glu His Thr Ala Glu
125 130 135

caa tgg ctc cca caa ttt ctc agt caa tta taatatttat tccctataca 786
Gln Trp Leu Pro Gln Phe Leu Ser Gln Leu
140 145

atggcatatg taaatcaa atgcccattt tcatactcgat caagcataat atttaaccaa 846

tcaaatcaat attttctctg tggataacta agatcaaaac tgtataaaag ctgttttat 906

tccctgaata agattgaatg tttttattc tgtggataac taaagaagtt attcacagtt 966

ttttctggtg ccaaatttgag atcttaacaa cttaaaaaat gatctaagtt attcatttaa 1026

aaaaagaaaa ggatcttaat cacagcacta taggatccta ataatcataa taataagatc 1086

tctttatata aaaagatcct atcttattt actcacgatc ttttcacga tcatacgatc 1146

gtcttgcataaaaatgtttc tttcatggat ccataaattt cagtagataa gccaaccagc 1206

aaaaaggatc aaaagatcca taaaatccga gataaattaa caaggttact atgtttata 1266

ctgaaaatta tgatgttatt gtgatcggtg gtggacacgc aggtactgaa gctgcacttg 1326

caccggcacg catgggactc aagaccctat tattaaccca taatgttgat acactaggc 1386

aaatgtcttg taatcctgcg attgggtggga ttggtaaagg ccatttagtc cgagaaattg 1446

atgcgatggg cggttaatg gcaactgctg cggaccaagc aggaatccaa tttcgatcc 1506

taaacagcag caaaggaccg gcggtacgtg ctacacgtgc gcaagctgac cgcgttttat 1566

atcgccaagc agtacgtatt gcattagaaa atcaagaaaa ttttagatatt tttcaacaag 1626

aagtgaccga tattattta gatcaggatc gtgtctgcgg tgggttact aaaatgggtt 1686
taaaattca cgcaaaagca gtgatttaa cagccggtaac ttcccttct ggtaagatcc 1746
acattggttt agaaaattat acaggtggac gcgcgggtga tcctgcttca gtgatgttag 1806
ccgatcgttt aagagaactg aatttacgtg tanatcgttt aaaaacgggt acaccgcccc 1866
gtattgatgc acgtactatt gatttctcaa tactggctaa acaacatggc gatgaaaaat 1926
tacctgtctt ttccatcgatg ggatctgtt atcaacaccc acgtcaaatt ccatgtttt 1986
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aagcaagggc gatgactggg ataaagtgcg tgatgtacaa gtaatggcg gcaatgagct 2526
gactgatatc acaaaaggat tgttatcggtt ctttattttt caatatcgcg caaccatgg 2586
tgagattcaa aactcggatt taaaagcaca agataaaagtc ga 2628

<210> 40
<211> 147
<212> PRT
<213> Pasteurella multocida

<400> 40
Met Lys Thr Lys Ile Cys Ile Ile Thr Gly Ser Thr Leu Gly Gly Ala
1 5 10 15
Glu Tyr Val Ala Glu His Ile Ala Glu Ile Leu Glu Gln Gln Asp Tyr
20 25 30
Pro Val Arg Leu Glu His Gly Pro Asn Phe Glu Glu Val Ile Asp Glu
35 40 45
Lys Cys Trp Leu Val Val Thr Ser Thr His Gly Ala Gly Glu Leu Pro
50 55 60
Asp Asn Ile Lys Pro Leu Phe Glu Lys Leu Ala Phe His Pro Lys Gln
65 70 75 80
Leu Ala Asp Leu Arg Phe Ala Val Ile Gly Leu Gly Asn Ser Asp Tyr
85 90 95
Asp Thr Phe Cys His Ala Val Asp His Val Glu Gln Leu Leu Leu Ser
100 105 110
Lys Asp Ala Leu Gln Leu Cys Glu Ser Leu Arg Met Asp Met Leu Thr

115	120	125
Ile Thr Asp Pro Glu His Thr Ala Glu Gln Trp Leu Pro Gln Phe Leu		
130	135	140
Ser Gln Leu		
145		

<210> 41
<211> 5191
<212> DNA
<213> *Pasteurella multocida*

<220>
<221> CDS
<222> (3203) .. (4255) .

<220>
<223> *mreB*

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tagcggttaa ttgggcagat ttatctttg gtactatcac agcacacacg cccgctgcat 180
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tgtttaaaaa ggcacttact gcatgaatgc cataaatatt ttcactcatc tactttctct 540
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cagcgtagcg tgcatttttc ttgagcttgc ctggctgtt tttgccttct cgtaatgggtt 720
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cacggatttt taccttacgt ccaatgcggt agatcatacc actattttca ccgattaaac 840
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tacattttt gatacatttgcacaattttca aatcagatgt tccatttattt 3180

aat tagttc agc gga attc tt atg tta ttt aaa aaa att cga ggc tta ttt	3232
Met Leu Phe Lys Lys Ile Arg Gly Leu Phe	
1 5 10	
tca aat gat ctg tcc atc gat ctt ggc aca gcg aat acc tta att tat	3280
Ser Asn Asp Leu Ser Ile Asp Leu Gly Thr Ala Asn Thr Leu Ile Tyr	
15 20 25	
gtc aaa gga caa ggg att gtt tta gat gaa cct tct gtt gtg gcg att	3328
Val Lys Gly Gln Gly Ile Val Leu Asp Glu Pro Ser Val Val Ala Ile	
30 35 40	
cgc caa gaa cgt tca ggt gca tta aaa agc att gct gcg gtt ggt cgt	3376
Arg Gln Glu Arg Ser Gly Ala Leu Lys Ser Ile Ala Ala Val Gly Arg	
45 50 55	
gat gcc aaa tta atg tta ggc cgt aca ccg aaa agc att gca gcg att	3424
Asp Ala Lys Leu Met Leu Gly Arg Thr Pro Lys Ser Ile Ala Ala Ile	
60 65 70	
cgt cct atg aaa gat ggg gtg atc gca gat ttc ttt gtg aca gaa aaa	3472
Arg Pro Met Lys Asp Gly Val Ile Ala Asp Phe Phe Val Thr Glu Lys	
75 80 85 90	
atg ttg caa tat ttt att aaa caa gtg cac agc agc aat ttt atg cgt	3520
Met Leu Gln Tyr Phe Ile Lys Gln Val His Ser Ser Asn Phe Met Arg	
95 100 105	
cca agt cca cgt gtc tta gtt tgt gta cct gcg gga gct acg caa gtc	3568
Pro Ser Pro Arg Val Leu Val Cys Val Pro Ala Gly Ala Thr Gln Val	
110 115 120	
gaa cga cgt gca atc aaa gaa tct gcc att ggt gct ggg gca cgc gag	3616
Glu Arg Arg Ala Ile Lys Glu Ser Ala Ile Gly Ala Gly Ala Arg Glu	
125 130 135	
gtg tac ttg att gag gaa ccg atg gcg gca gcg att ggt gct aaa tta	3664
Val Tyr Leu Ile Glu Glu Pro Met Ala Ala Ile Gly Ala Lys Leu	
140 145 150	
cct gtt tcg act gcc aca ggt tcg atg gtg atc gat atc ggt ggt ggt	3712
Pro Val Ser Thr Ala Thr Gly Ser Met Val Ile Asp Ile Gly Gly Gly	
155 160 165 170	
acg acg gaa gtt gcg gtg att tct tta aat ggc att gtg tat tcc tct	3760
Thr Thr Glu Val Ala Val Ile Ser Leu Asn Gly Ile Val Tyr Ser Ser	
175 180 185	
tca gtc cgc att ggt ggt gat cgt ttt gat gag gcg att att tct tat	3808
Ser Val Arg Ile Gly Gly Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr	
190 195 200	
gta cgc aag acg ttc ggt tca att att ggg gaa ccg aca gca gag cgt	3856
Val Arg Lys Thr Phe Gly Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg	
205 210 215	
atc aaa caa gag att ggt agt gcg ttt att caa gaa ggc gat gaa gtc	3904
Ile Lys Gln Glu Ile Gly Ser Ala Phe Ile Gln Glu Gly Asp Glu Val	
220 225 230	
cgt gaa att gaa gtg cat ggt cat aac tta gca gaa ggt gcg ccg cgt	3952
Arg Glu Ile Glu Val His Gly His Asn Leu Ala Glu Gly Ala Pro Arg	
235 240 245 250	

tct ttc aaa ctc acc tca cgt gat gtg tta gaa gct att caa gcc ccg	4000
Ser Phe Lys Leu Thr Ser Arg Asp Val Leu Glu Ala Ile Gln Ala Pro	
255 260 265	
tta aat ggc att gtt gcg gca gtg cgc acg gcc ttg gaa gag tgt caa	4048
Leu Asn Gly Ile Val Ala Ala Val Arg Thr Ala Leu Glu Glu Cys Gln	
270 275 280	
cca gaa cat gct gcg gat att ttt gaa cgt ggc atg gtc tta act ggt	4096
Pro Glu His Ala Ala Asp Ile Phe Glu Arg Gly Met Val Leu Thr Gly	
285 290 295	
ggc ggt gcc ctt att cgt aat att gat gtt tta ctg tca aaa gaa acc	4144
Gly Gly Ala Leu Ile Arg Asn Ile Asp Val Leu Leu Ser Lys Glu Thr	
300 305 310	
ggt gtg ccg gtt atc atc gcc gat gat cct tta acc tgt gtt gcc cgt	4192
Gly Val Pro Val Ile Ile Ala Asp Asp Pro Leu Thr Cys Val Ala Arg	
315 320 325 330	
ggt ggt ggc gag gca tta gag atg atc gat atg cac ggt ggt gat att	4240
Gly Gly Glu Ala Leu Glu Met Ile Asp Met His Gly Gly Asp Ile	
335 340 345	
ttt agt gac gat atc taatatgatt taaaagtgcg gtgatattag accgcactt	4295
Phe Ser Asp Asp Ile	
350	
taattcttta ttattgctga caaggctagc ctaattcgta tatgaaacct atttttggaa	4355
aaggcacctcc tttaggtctt cgcttaattc tggcgatttt agcatccatt gcattgattt	4415
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gtaatgatgt ccgtttgatt gctagtggaa caggacggaa tcatgtactg agtttagatc	4955
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ggcgttttt agaaggttat cctgttgcca ttgtgaaatc cgtatcacgt gatgggcaaa	5075
attatatttgc tactgttaaca gcaaagccat tagcttcgtat tgaacgttta cgctatgtt	5135
tgctttatg gccgacgaat gaagagatgc gcaaagtcca gtctatttca cctgca	5191

<210> 42
<211> 351
<212> PRT
<213> Pasteurella multocida

<400> 42
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Asp Leu Gly Thr Ala Asn Thr Leu Ile Tyr Val Lys Gly Gln Gly Ile
20 25 30
Val Leu Asp Glu Pro Ser Val Val Ala Ile Arg Gln Glu Arg Ser Gly
35 40 45
Ala Leu Lys Ser Ile Ala Ala Val Gly Arg Asp Ala Lys Leu Met Leu
50 55 60
Gly Arg Thr Pro Lys Ser Ile Ala Ala Ile Arg Pro Met Lys Asp Gly
65 70 75 80
Val Ile Ala Asp Phe Phe Val Thr Glu Lys Met Leu Gln Tyr Phe Ile
85 90 95
Lys Gln Val His Ser Ser Asn Phe Met Arg Pro Ser Pro Arg Val Leu
100 105 110
Val Cys Val Pro Ala Gly Ala Thr Gln Val Glu Arg Arg Ala Ile Lys
115 120 125
Glu Ser Ala Ile Gly Ala Gly Ala Arg Glu Val Tyr Leu Ile Glu Glu
130 135 140
Pro Met Ala Ala Ala Ile Gly Ala Lys Leu Pro Val Ser Thr Ala Thr
145 150 155 160
Gly Ser Met Val Ile Asp Ile Gly Gly Thr Thr Glu Val Ala Val
165 170 175
Ile Ser Leu Asn Gly Ile Val Tyr Ser Ser Ser Val Arg Ile Gly Gly
180 185 190
Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr Val Arg Lys Thr Phe Gly
195 200 205
Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg Ile Lys Gln Glu Ile Gly
210 215 220
Ser Ala Phe Ile Gln Glu Gly Asp Glu Val Arg Glu Ile Glu Val His
225 230 235 240
Gly His Asn Leu Ala Glu Gly Ala Pro Arg Ser Phe Lys Leu Thr Ser
245 250 255
Arg Asp Val Leu Glu Ala Ile Gln Ala Pro Leu Asn Gly Ile Val Ala
260 265 270
Ala Val Arg Thr Ala Leu Glu Glu Cys Gln Pro Glu His Ala Ala Asp
275 280 285
Ile Phe Glu Arg Gly Met Val Leu Thr Gly Gly Ala Leu Ile Arg
290 295 300
Asn Ile Asp Val Leu Leu Ser Lys Glu Thr Gly Val Pro Val Ile Ile
305 310 315 320
Ala Asp Asp Pro Leu Thr Cys Val Ala Arg Gly Gly Gly Glu Ala Leu
325 330 335

Glu Met Ile Asp Met His Gly Gly Asp Ile Phe Ser Asp Asp Ile
340 345 350

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Thr Arg Val Gly Ile Gly Trp His Leu Asn Pro Asn Thr Ala Leu Ile
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gaa aaa gtg aaa gcg att gca gaa gcg cgt tta ggc gaa gca tac cgt 96
Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly Glu Ala Tyr Arg
20 25 30

atc act gaa aac aag cac gtt atg aac aaa att gat gcg att aaa gct 144
Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala
35 40 45

gat gtg att gca caa atc aca gct gaa gta gca gaa ggc gaa gac atc 192
Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile
50 55 60

agt gaa ggg aaa att gtc gat att ttc acc gca ctt gaa agc caa atc 240
Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile
65 70 75 80

gta cgt agc cgt atc att gct ggt gaa cca cgt att gat ggt cgt aca 288
Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr
85 90 95

gtg gat act gtt cgt gca tta gat att tgt act ggt gtt tta cca cgt 336
Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg
100 105 110

aca cac ggt tct gcg att ttc acc cgt ggt gaa aca cag gcg tta gct 384
Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala
115 120 125

gtc gcg aca tta ggt aca gaa cgt gat gca caa att att gat gaa tta 432
Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu
130 135 140

aca ggt gag cgt tca gat cac ttc tta ttc cac tac aac ttc ccg cca 480
Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr Asn Phe Pro Pro
145 150 155 160

tat tct gtg ggt gaa acc ggt atg att ggt tca cca aaa cgt cgt gaa 528
Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro Lys Arg Arg Glu
165 170 175

att ggt cat ggt cgt tta gcg aaa cgc ggt gta gct gca gtg atg cca 576
Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala Ala Val Met Pro

180	185	190	
aca ctt gcc gag ttc ccg tat gtg gta cgt gtt gtc tct gaa atc aca			624
Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr			
195	200	205	
gaa tca aat ggt tct tct atg gca tcg gtt tgt ggt gcg tct tta			672
Glu Ser Asn Gly Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu			
210	215	220	
gca tta atg gat gcg ggt gta cca att aaa gcg gcg gtt gca ggt att			720
Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile			
225	230	235	240
gca atg ggc tta gtc aaa gaa gac gaa aaa ttt gtg gtg ctt tca gac			768
Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp			
245	250	255	
atc tta ggt gat gaa gat cac tta ggt gac atg gac ttc aaa gtc gcg			816
Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala			
260	265	270	
ggt aca cgt acg ggt gtg acg gca tta caa atg gat atc aaa atc gaa			864
Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu			
275	280	285	
ggt atc aca gca gaa atc atg caa att gcg tta aac caa gcg aaa agc			912
Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn Gln Ala Lys Ser			
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gca cgt tta cac att tta ggt gtg atg gag caa gcg atc cca gcg cca			960
Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro			
305	310	315	320
cgt gcg gat att tct gat ttt gca ccg cgt att tac act atg aaa att			1008
Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile			
325	330	335	
gat ccg aag aaa atc aaa gat gtg atc ggt aaa ggt ggt gca acc att			1056
Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Ala Thr Ile			
340	345	350	
cgt gcc tta aca gaa gaa aca ggt acc tca att gat atc gat gat gat			1104
Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp Ile Asp Asp Asp			
355	360	365	
ggt acg gtg aag att gct gcg gtt gat ggc aat tca gca aaa gag gtg			1152
Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser Ala Lys Glu Val			
370	375	380	
atg gcg cgt att gaa gat att act gca gaa gtt gaa gcg ggt gca gtg			1200
Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val			
385	390	395	400
tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt gcc ttc gtt tct			1248
Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser			
405	410	415	
atc gta ggt aac aaa gaa ggc tta gtg cat att tct caa atc gcg gaa			1296
Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu			
420	425	430	
gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg ggg caa gaa gtg			1344

Glu	Arg	Val	Glu	Lys	Val	Ser	Asp	Tyr	Leu	Ala	Val	Gly	Gln	Glu	Val
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act	gtt	aaa	gtg	gtt	gag	att	gat	cgt	caa	ggt	cgt	att	cgt	tta	acc
Thr	Val	Lys	Val	Val	Glu	Ile	Asp	Arg	Gln	Gly	Arg	Ile	Arg	Leu	Thr
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Met	Lys	Glu	Val	Ala	Pro	Lys	Gln	Glu	His	Val	Asp	Ser	Val	Val	Ala
465						470					475				480
gac	gtt	gcc	gca	gaa	gaa	aac	gca	taagcaataa	acaccaacgc	ccttcgtat					1494
Asp	Val	Ala	Ala	Glu	Glu	Asn	Ala								
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acagcgcac	tctagatatc	tttaatgtgt	tgtttgaact	tgatcctcaa	tatgagtatg										1974
cattcctaaa	tagagggcta	aattttatt	acgtcggacg	ttatgaatta	gctcagcggg										2034
attttcttca	attttatcaa	gccgataaat	cagatccata	ccgcacttta	tggcttatt										2094
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Ile	Thr	Glu	Asn	Lys	His	Val	Met	Asn	Lys	Ile	Asp	Ala	Ile	Lys	Ala
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Asp	Val	Ile	Ala	Gln	Ile	Thr	Ala	Glu	Val	Ala	Glu	Gly	Glu	Asp	Ile
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Ser	Glu	Gly	Lys	Ile	Val	Asp	Ile	Phe	Thr	Ala	Leu	Glu	Ser	Gln	Ile
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Val	Arg	Ser	Arg	Ile	Ile	Ala	Gly	Glu	Pro	Arg	Ile	Asp	Gly	Arg	Thr
						85					90			95	

Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg
100 105 110

Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala
115 120 125

Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu
130 135 140

Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr Asn Phe Pro Pro
145 150 155 160

Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro Lys Arg Arg Glu
165 170 175

Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala Ala Val Met Pro
180 185 190

Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr
195 200 205

Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu
210 215 220

Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile
225 230 235 240

Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp
245 250 255

Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala
260 265 270

Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu
275 280 285

Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn Gln Ala Lys Ser
290 295 300

Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro
305 310 315 320

Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile
325 330 335

Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile
340 345 350

Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp Ile Asp Asp Asp
355 360 365

Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser Ala Lys Glu Val
370 375 380

Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val
385 390 395 400

Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser
405 410 415

Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu
420 425 430

Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val
435 440 445

Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr
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Asp Val Ala Ala Glu Glu Asn Ala
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Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val
20 25 30

gtc att cct gtg cct gaa acc tct aac gat att gct tta cgt att gcg 145
Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala
35 40 45

cgc gtg tta aat aaa ccg tat cgt caa ggt ttt gtg aaa aat cgc tat 193
Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr
50 55 60

gta gga cgt acg ttt att atg ccg ggg cag gca ttg cga gtc agt tct 241
Val Gly Arg Thr Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser
65 70 75 80

gtt aga cgt aaa ctc aat acc att gct tca gaa ttt aaa gat aag aat 289
Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn
85 90 95

gtg tta tta gtt gac gac tcg att gta cgt ggt acc acg tct gaa caa 337
Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln
100 105 110

att gtc gaa atg gcg aga gcg gca ggt gcg aag aaa att tat ttt gcc 385
Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala
115 120 125

tct gct gca cca gaa att cgt tat cca aat gtg tat ggt att gat atg 433
Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met
130 135 140

cca acc aaa aat gaa ttg atc gct tat ggt cgt gat gta gat gaa att 481

Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile
145 150 155 160

gct aac tta att ggt gtg gat aaa ttg att ttc caa gat ttg gat gcg 529
Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala
165 170 175

tta act ggt tct gtg caa caa gaa aat cca agt att caa gac ttt gat 577
Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp
180 185 190

tgt tcg gtg ttt aca ggg gtt tat gtg acg ggc gat att aca cct gaa 625
Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu
195 200 205

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Tyr Leu
210

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Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala
35 40 45

Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr
50 55 60

Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser
65 70 75 80

Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn
85 90 95

Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln
100 105 110

Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala
115 120 125

Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met
130 135 140

Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile
145 150 155 160

Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala
165 170 175

Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp
180 185 190

Cys Ser Val Phe Thr Gly Val Tyr Gly Asp Ile Thr Pro Glu

195

200

205

Tyr Leu
210

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att att ttt aga gat gta ata gaa cgc tat caa aat gaa gtg tct ata 96
Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile
20 25 30

act aaa aaa ggc gcg cga aat gaa att ata aga tta aac cgc ttt tta 144
Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu
35 40 45

aga tat gat att tct aat ctg tat att cgt gat tta aga aaa gaa gat 192
Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp
50 55 60

ttt gag gag tgg atc aga att cgc cta acc gaa gta tcg gat gct agc 240
Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser
65 70 75 80

gtt aga cgt gag ctt gtt act ata tcg tca gtg ctg aca aca gca ata 288
Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile
85 90 95

aat aag tgg gga tat att tca agg cat cca atg act ggt att gaa aaa 336
Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met Thr Gly Ile Glu Lys
100 105 110

cca aaa aac tcg gca gaa aga aaa gaa cga tat tca gaa cag gac att 384
Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr Ser Glu Gln Asp Ile
115 120 125

aaa aca ata tta gaa aca gct aga tat tgt gaa gat aaa cta ccc ata 432
Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu Asp Lys Leu Pro Ile
130 135 140

aca ctc aaa caa aga gta gca att gca atg tta ttt gct att gaa acc 480
Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu Phe Ala Ile Glu Thr
145 150 155 160

gct atg cgt gct ggt gag att gct agt ata aaa tgg gat aat gtt ttt 528

Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys Trp Asp Asn Val Phe
 165 170 175
 ctt gaa aag aga ata gta cat tta ccg aca act aaa aac ggg cac tct 576
 Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr Lys Asn Gly His Ser
 180 185 190
 aga gat gtg ccg ctt tcg caa aga gct gtt gcg cta att tta aaa atg 624
 Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala Leu Ile Leu Lys Met
 195 200 205
 aaa gag gta gaa aat gga gat ctt gtg ttt cag acc acg cct gaa tca 672
 Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln Thr Thr Pro Glu Ser
 210 215 220
 tta agc acc acg ttt aga gtg tta aag aaa gag tgt gga ctt gaa cat 720
 Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu Cys Gly Leu Glu His
 225 230 235 240
 ctc cat ttt cat gat acg aga agg gaa gcg ttg acg aga tta tct aag 768
 Leu His Phe His Asp Thr Arg Arg Glu Ala Leu Thr Arg Leu Ser Lys
 245 250 255
 aaa gta gat gta atg act cta gcc aaa att agc gga cat aga gat tta 816
 Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser Gly His Arg Asp Leu
 260 265 270
 aga att tta caa aac aca tat tac gca ccg aat atg agt gaa gtg gca 864
 Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn Met Ser Glu Val Ala
 275 280 285
 aac ttg ttg gat taattcactc ttcttaataa cgcctttgc cacttgatta 916
 Asn Leu Leu Asp
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cgtgctgtct tgattgatat aatcaattaa tctaagccca atccattca taactggAAC 3736
agccatactg tttccaattg ctttgtatcg tggagaatca gggcattcat ctattgattt 3796
gttgcgatat gggatttttag tgtaatcgTC tgaaaatccc tgtaatctt cacactcACG 3856
cggcgtagt tttctaacaa ctgattctac tgataaAGCA acgcaaggAA cattattacc 3916
accagttccc attcttgctt ttaaggTTgg tgaaatatca tcgtgaatac gacaagcttc 3976
ttcacccTTA acctcaaata gaatatttc caatcctca tttcttccaa tgcaatgcgc 4036
tgtatTTTA gaaatgattg gatcttgcA accgtgaaca acaaaAGTTT cactaccGCC 4096
agcaagaact ccaccgcttg ctcttaatgt tcccgcaaca tcggatttgc gatattgagc 4156
aaagcttgc tcaataaagg cggcaatATC tttgcctgc gttccgctct gttcaatatt 4216
ccctcgacG ctTTTggact caatgagTAT ttgtgcaaca cttcgTTTC tagcacttgc 4276
cacaagaaac actctttac gacgTTggc aactccgaag tattgagcat cgagaactcg 4336
ccagcagatt gttcggattg aatgcacata accagcgttc gtccatcttc tccctgtgt 4396
ctgcaatggc tcacactctt gaaccagtcc agccagaagg tgtccgaatg cgTTgtccga 4456
ggTggatAGC acacccggaa cgTTTccca cacgagaatg cacggTggTT tgTTgtcatt 4516
gaatctaaca tagtcgatcg ctTctaaaat tttaattaaa actaacgtga gatttcctcg 4576
ctcatcgTct aaactttgac gattgccAGC aactgaaaaa gattgacaag gagtaccacc 4636
aactaaaacg tctggTgCCG gaatttcacG atctaataatt ttctgttgca attcagtcat 4696
atcaccaaga ttgggaacgt tagggtaatg gtaagctaAt actgcgcttg ggaattgctc 4756
aatttcagaa aaccagagtG gctctgcgaa tt 4788

<210> 48
<211> 292
<212> PRT
<213> Pasteurella multocida

<400> 48
Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys Gly Ile Ala Pro Asp
1 5 10 15
Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile
20 25 30
Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu
35 40 45
Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp
50 55 60
Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser
65 70 75 80
Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile
85 90 95

Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met Thr Gly Ile Glu Lys
100 105 110

Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr Ser Glu Gln Asp Ile
115 120 125

Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu Asp Lys Leu Pro Ile
130 135 140

Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu Phe Ala Ile Glu Thr
145 150 155 160

Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys Trp Asp Asn Val Phe
165 170 175

Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr Lys Asn Gly His Ser
180 185 190

Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala Leu Ile Leu Lys Met
195 200 205

Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln Thr Thr Pro Glu Ser
210 215 220

Leu Ser Thr Thr Phe Arg Val Leu Lys Glu Cys Gly Leu Glu His
225 230 235 240

Leu His Phe His Asp Thr Arg Arg Glu Ala Leu Thr Arg Leu Ser Lys
245 250 255

Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser Gly His Arg Asp Leu
260 265 270

Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn Met Ser Glu Val Ala
275 280 285

Asn Leu Leu Asp
290

<210> 49
<211> 1618
<212> DNA
<213> *Pasteurella multocida*

<220>
<221> CDS
<222> (2)..(1195)

<220>
<223> *sopE*

<400> 49
g ggc gat cta tgt ctg aaa ata tct aca tgg tgt caa agt cac aga atc 49
Gly Asp Leu Cys Leu Lys Ile Ser Thr Trp Cys Gln Ser His Arg Ile
1 5 10 15

aat caa gca att cgc aca att caa agt cta tca acc gca gtc atc ggt 97
Asn Gln Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly
20 25 30

att gtc tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat 145
Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn

35	40	45	
gaa ccc gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly	50	55	193
		60	
aaa caa ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val	65	70	241
		75	80
aat tgc aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp	85	90	289
		95	
gaa gaa aca aaa gca agt gaa atg aac acg gca att att ggc aca atc Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile	100	105	337
		110	
aca gaa gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa Thr Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Ile Ala Lys	115	120	385
		125	
aac aaa ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp	130	135	433
		140	
aca aaa gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn	145	150	481
		155	160
gca ttt gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala	165	170	529
		175	
gtg caa tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met	180	185	577
		190	
ggc gat ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp	195	200	625
		205	
tat gcc gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa Tyr Ala Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu	210	215	673
		220	
cag ggc tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser	225	230	721
		235	240
ggt gtc aca caa cca ctc tat ttt gac att aac gac agc tcg act gat Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp	245	250	769
		255	
gtg aac tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn	260	265	817
		270	
ggc ttt cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe	275	280	865
		285	
aag ttt gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att			913

Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile
290 295 300

gca ggg gcg ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta 961
Ala Gly Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu
305 310 315 320

gtg aaa gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc 1009
Val Lys Asp Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr
325 330 335

aca aaa ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt 1057
Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu
340 345 350

aac agt gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat 1105
Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp
355 360 365

tat cac cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att 1153
Tyr His Pro Val Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile
370 375 380

tct gat gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg 1195
Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
385 390 395

taagggtag aaaatggctt taccacgcaa acttaaattt atgaatttaa tcatcgacgg 1255

taacaaatat ctcggcgaag tcacggaagt gactcaacca aaatttagcaa tgaaaatcga 1315

agaatttcgc gcgggcggta tgattggttc ggtggatgtc aatctcgggc ttgaaaagct 1375

cgaagcggaa tttaaagccg gtggctacat ggtcgaatta attaaaaat tcggcgggtc 1435

aatcaacggc attccattgc gtttcttgg ctcatatcag cgtgatgaca cagaagaagt 1495

cacatctgtt gagcttgtga tgcaaggctcg atttactgaa attgacagcg gaaacagcaa 1555

agtggcgat gacactgaac aaacattcaa agtgccttta acgtattaca aaatcattgt 1615

tga 1618

<210> 50
<211> 398
<212> PRT
<213> Pasteurella multocida

<400> 50
Gly Asp Leu Cys Leu Lys Ile Ser Thr Trp Cys Gln Ser His Arg Ile
1 5 10 15

Asn Gln Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly
20 25 30

Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn
35 40 45

Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly
50 55 60

Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val

65	70	75	80
Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp			
85		90	95
Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile			
100		105	110
Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys			
115		120	125
Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp			
130		135	140
Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn			
145		150	160
155			
Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala			
165		170	175
Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met			
180		185	190
Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp			
195		200	205
Tyr Ala Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu			
210		215	220
Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser			
225		230	240
235			
Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp			
245		250	255
Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn			
260		265	270
270			
Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe			
275		280	285
Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile			
290		295	300
300			
Ala Gly Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu			
305		310	320
315			
Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr			
325		330	335
335			
Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu			
340		345	350
350			
Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp			
355		360	365
365			
Tyr His Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile			
370		375	380
380			
Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser			
385		390	395
395			

<210> 51
<211> 353
<212> DNA
<213> *Pasteurella multocida*

<220>
<221> CDS
<222> (1)..(351)

<220>
<223> unknown C1

<400> 51
atg aca tta ttt gat gaa tgt aaa tta gct ctt aga gac gat ttt aat 48
Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
1 5 10 15
ctt att tgt gat gaa gag aag gat tgt gta atg gat aag ttt tat ttc 96
Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
20 25 30
tat ttc ttg gaa aag aaa gag gaa ttt aat ttt caa gat tat tca ttt 144
Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
35 40 45
gaa gaa atg tat ata ttt tca aaa atg gaa cct gtg tat gtt tta tgt 192
Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
50 55 60
gat agc tct aat ata cct ttg ttt agg agt aat tgg gaa ttg att atc 240
Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
65 70 75 80
aat aat ata tat gat gtt gtc tgt tta tct aca aaa gta ttt ttt cta 288
Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
85 90 95
gat gat gaa aag tta atg atg gaa tta ttt cct gaa gat aaa gta aga 336
Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
100 105 110
gtc atc tat aaa aga ta 353
Val Ile Tyr Lys Arg
115

<210> 52
<211> 117
<212> PRT
<213> *Pasteurella multocida*

<400> 52
Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
1 5 10 15
Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
20 25 30
Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
35 40 45
Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
50 55 60

Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
65 70 75 80

Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
85 90 95

Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
100 105 110

Val Ile Tyr Lys Arg
115

<210> 53
<211> 509
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1)..(507)

<220>
<223> unknown C2

<400> 53
atg aaa aat ttt agg aat ata aat att tat agt gat tat gga aag gtt 48
Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val
1 5 10 15

gat aag gaa att ata tta gaa ttc gaa aat gaa ttt aat ata aag ctt 96
Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu
20 25 30

cct tct tta tac ata gat tta att acg gcg cat aat gct ccg aag agt 144
Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser
35 40 45

gaa gag aat tgc ttt gaa tat tac aat gag cgt aat gag ccc acg ttt 192
Glu Glu Asn Cys Phe Glu Tyr Tyr Asn Glu Arg Asn Glu Pro Thr Phe
50 55 60

tct tcc ttt gga ttt gaa ggg ttt gag aca gag cgg tct agc gcc tct 240
Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Arg Ser Ser Ala Ser
65 70 75 80

ctt gaa aat ata tat gct cag tat att tat gat gat cca atc tat ggt 288
Leu Glu Asn Ile Tyr Ala Gln Tyr Ile Tyr Asp Asp Pro Ile Tyr Gly
85 90 95

tat gaa cat gtg tat tct ttt ggt agt act ggc gag gga cat ttt atc 336
Tyr Glu His Val Tyr Ser Phe Gly Ser Thr Gly Glu Gly His Phe Ile
100 105 110

tgt ttt gat tat cgt gat gat cca aaa ggt gat gaa ccc aaa atc tgt 384
Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys
115 120 125

atc gtg att cac gat gaa tat gat gaa aaa aca ggg aaa atg cga ctg 432
Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu
130 135 140

ttt cct ata gca gag aat ttt gaa gcg ttt tta gat agt ttg aaa tca 480

Phe Pro Ile Ala Glu Asn Phe Glu Ala Phe Leu Asp Ser Leu Lys Ser
145 150 155 160

ttt gat gaa atg ata gag aag tat tcg ta 509
Phe Asp Glu Met Ile Glu Lys Tyr Ser
165

<210> 54
<211> 169
<212> PRT
<213> Pasteurella multocida

<400> 54
Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val
1 5 10 15

Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu
20 25 30

Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser
35 40 45

Glu Glu Asn Cys Phe Glu Tyr Tyr Asn Glu Arg Asn Glu Pro Thr Phe
50 55 60

Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Arg Ser Ser Ala Ser
65 70 75 80

Leu Glu Asn Ile Tyr Ala Gln Tyr Ile Tyr Asp Asp Pro Ile Tyr Gly
85 90 95

Tyr Glu His Val Tyr Ser Phe Gly Ser Thr Gly Glu Gly His Phe Ile
100 105 110

Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys
115 120 125

Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu
130 135 140

Phe Pro Ile Ala Glu Asn Phe Glu Ala Phe Leu Asp Ser Leu Lys Ser
145 150 155 160

Phe Asp Glu Met Ile Glu Lys Tyr Ser
165

<210> 55
<211> 443
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> unknown C3

<400> 55
atg ata aaa tat tta gag gga aat att aac tcg ttt ata tcg gca tta 48
Met Ile Lys Tyr Leu Glu Gly Asn Ile Asn Ser Phe Ile Ser Ala Leu

1	5	10	15	
ggt aaa aac gaa agt aat aaa gat att tta aaa tta gta gaa ata gtt				96
Gly Lys Asn Glu Ser Asn Lys Asp Ile Leu Lys Leu Val Glu Ile Val				
20	25	30		
tct tca gat ttt gaa gtg gat gaa cta agt cat aaa gat gaa cac gag				144
Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu				
35	40	45		
ata tat tat ttg ttt tat aag agg ggt gtt gaa ttt tgt ttt aaa aga				192
Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg				
50	55	60		
ata gat gaa gag tat gtc tta tat tcg gtt ttc ttt ttc ttg gta gag				240
Ile Asp Glu Glu Tyr Val Leu Tyr Ser Val Phe Phe Leu Val Glu				
65	70	75	80	
gtt gat aat tat ttt tca tgc cca ttt att cat gaa tta ata tgt gat				288
Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp				
85	90	95		
ctt aaa cac gga ttc tca ata gag gat att ata agg ttt tta ggg gag				336
Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu				
100	105	110		
cca aat ttt aaa ggt agt ggc tgg gta aga tat tct tat aat gga aga				384
Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg				
115	120	125		
aat att cat ttc gaa ttt aat gaa tct aat gaa tta tcc cag att agc				432
Asn Ile His Phe Glu Phe Asn Glu Ser Asn Glu Leu Ser Gln Ile Ser				
130	135	140		
att ttt att ta				443
Ile Phe Ile				
145				
<210> 56				
<211> 147				
<212> PRT				
<213> Pasteurella multocida				
<400> 56				
Met Ile Lys Tyr Leu Glu Gly Asn Ile Asn Ser Phe Ile Ser Ala Leu				
1	5	10	15	
Gly Lys Asn Glu Ser Asn Lys Asp Ile Leu Lys Leu Val Glu Ile Val				
20	25	30		
Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu				
35	40	45		
Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg				
50	55	60		
Ile Asp Glu Glu Tyr Val Leu Tyr Ser Val Phe Phe Leu Val Glu				
65	70	75	80	
Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp				
85	90	95		

Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu
100 105 110

Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg
 115 120 125

Asn	Ile	His	Phe	Glu	Phe	Asn	Glu	Ser	Asn	Glu	Leu	Ser	Gln	Ile	Ser
130						135					140				

Ile Phe Ile
145

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<210> 57
<211> 8498
<212> DNA
<213> Pasteurella multocida
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<220>
<223> unknown C

<400> 57
gaattcgaat taagcgagaa aattgctgaa acactagaac aaagtcaatt aaatattagt 60
caattatcaa ttgttggaaat ttatccttgc aatgaagaac aagggatacg ttttcataat 120
aaaagtgtgg tacaacttaa accagaagag gtggaatggc catcaatcca ttatctttc 180
tttgctggcg atattcagca agtcgctcat ctcgcgaaag ccgcagaaat gggttgcgtg 240
gtgattgata tgaaagggat ttgtgccagc ttgcaagacg tccctgtggt gataccggga 300
gtaaatcagg aaaaattggt agatttacgt cagcgtataa ttgtgtcctt agccgatcca 360
caagtgacac aacttgcatt agtcatcgcc tcggtgatgt caaatcacga aatcaaagac 420
attgccgtaa cctcggttatt acctgcatct tatactaacg gagaaacggt aggtaaattt 480
gcgggacaaa cagcgcgatt gttaaatggc attccacttg atgaaggcga acaacgttta 540
gctttgatg ttttccctac gcctgcatcg catttaaata tgcaaattca caagatcttt 600
ccacaattag ataatgtcgt atttcattct atccaagtgc ctgtttctt cgggatgggg 660
caaatggta gcgtattatc ggattatgca ttagatcctc aatcttgctt agcgagctgg 720
actgacaatc cggtgatgac ttatcatgca gaaaaatatt gcaccccgat gacgaatggc 780
gaacaggaaa tggcagaaga gcaagcagca aaattacata taagtgggtt aagtgcggcg 840
gaaaatggtc tacaattttg gtcgggttgc gatgaacagc gcttaatct tgctttattt 900
agtgttacgc ttgcagagtt aatttactcg caagggttatt aatttaatg tgtttttgc 960
cgatattttt atcttgaact ttgagagcgc actcggtttt gacgagtgcg tttttgtttaa 1020
aacattcgtt tgaaagacag tgaatgaata gcggagttat tgataagaat caatttatac 1080
aaaagcaact gaatgttatt aatcgaggca ataaacctat tgatagttt agttggcgcc 1140
ataatacata aactgtactt aataatatgc aatcaataacc tagaaatatt catgacgtaa 1200
tccaaacatata cggggggggggg attttaaqtq atqqtqaaaa aaacatttaq aaatctaaaa 1260

atatatgatg attatggttc tgtctctcag gaaatttattt ttaattttga aaaagagttt 1320
gatataaaaac tccctttatc ctatatctca cttgtgaaaa agtataatgg cgtttggttt 1380
aaggaaaagtg attttgaata tttatctcaa aatgggaaaa gaataataag ctcattgagt 1440
tttgatagtt ttgagacaaa agataatatc gaaccaatga ataatatatt aagacaatat 1500
atttatgatg atgaaattta tggatataag aatgtttattt cctttggta cactggaaat 1560
ggtgactttg tctgtttga ttatcgtat gacccaaaag gtatgagcc caaaatctgt 1620
atcgtgattc atgatgaata tcatgaaaaa acaggcaagc gtttgttattt gcctgtggca 1680
gaaaattttg aggcatttt agatatgctt tacgattttg atgaacgcta tccgaatgg 1740
tatgaatagg tatttggtaa aataatgtgt ttttattttt aagcattatt tacaactaac 1800
attttaagtg cggtaattt tgaaaaagtt ttgggctttg agaattggc gcatttttt 1860
tcaaataattc ttcaatgatg agcactaattt atggattaga taatggaaat tatcgagata 1920
tggatggtaa taaaggatgg aggctagatt ttgatcctga gaaagttgtt catgtaaata 1980
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tt 5798

<210> 59
<211> 587
<212> PRT
<213> Pasteurella multocida

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20 25 30
Ala Phe Pro Leu Leu Val Leu Ile Gly Phe Thr Val Asp Gly Thr Gly
35 40 45
Val Val Leu Asp Lys Ala Arg Leu Ala Gln Gly Met Asp Gln Ala Ala
50 55 60
Leu Ala Leu Val Ala Glu Asn Asn Asp Tyr Arg Glu Asn Lys Lys His
65 70 75 80
Gly Asp Val Asn Arg Gln Val Val Ser Pro Gln Asp Lys Ala Lys Phe
85 90 95
Gly Gly Asn Glu Phe Met Ala Lys Gln Glu Lys Arg Asn Gln Glu Leu
100 105 110
Ile Gln Gly Ile Ala Lys Leu Tyr Leu Arg Ser Glu Asn Ala Asn Ala

115	120	125
Ser Ser Asp Ala Pro Ile Thr Ile Asp Lys Pro Phe His Tyr Ser Cys		
130	135	140
Glu Glu Leu Asp Leu Pro Thr Ala Asn Glu Tyr Ala Arg Arg Lys Pro		
145	150	155
160		
Ile Val Cys Glu Val Gln Gly Gly Val Asn Arg Lys Phe Trp Leu Pro		
165	170	175
Val Ser Glu Ser Leu Val Ser Glu Asp Lys Leu Lys Lys Asp Arg Val		
180	185	190
Arg Leu Glu Ser Asp Thr Ser Tyr Ala Ile Lys Glu Lys Gly Ile Val		
195	200	205
Ile Pro Val Glu Leu Met Leu Val Ser Asp Tyr Ser Gly Ser Met Asn		
210	215	220
Ser His Leu Gln Asp Lys Asn Gly Arg Ser Leu Gly Lys Ala Lys Ile		
225	230	235
240		
Thr Ile Leu Arg Glu Val Val Ser Glu Ile Ser Lys Ile Leu Leu Pro		
245	250	255
Glu Asp Val Ser Glu Gly Val Ser Pro Phe Asn Arg Ile Gly Phe Thr		
260	265	270
Thr Phe Ser Gly Gly Val Arg Gln Arg Asp Val Thr Glu Gly Cys Val		
275	280	285
Leu Pro Tyr Glu Gly Lys Ile Ser Gln Thr Ser Arg Lys Leu Thr Ile		
290	295	300
Arg Tyr Trp Ile Thr Gly Asn Asn Thr Pro Trp Lys Phe Asn Ala Gly		
305	310	320
Arg Trp Glu Arg Ser Thr Val Ser Phe Gln Glu His Tyr Lys Gly Tyr		
325	330	335
Tyr Asp Lys Phe His Ser Ser Thr Cys Arg Gly Ser Gly Ser Ser Arg		
340	345	350
Thr Cys Gln Ile Asp Ala Asn Pro Lys Lys Ile Met Asp Tyr Ala Leu		
355	360	365
Lys Ile Asn Asp Trp Thr Thr Ile Arg Glu Leu Phe Asn Thr Tyr Ile		
370	375	380
Asp Val Ser Gly Thr Ile Asp Gln Ile Ser Gln Phe Asp Gly Ser Asn		
385	390	395
400		
Arg Arg Tyr Asp Met Val Phe Thr Asp Glu Glu Arg Cys Leu Gly Gly		
405	410	415
Asn Ile Gly Arg Arg Thr Thr Arg Ala Trp Phe Asp Gln Lys Asn Lys		
420	425	430
Asp Ile Thr Arg Glu Leu Asn Ile Val Arg Pro Ser Gly Trp Thr Ser		
435	440	445
Ala Ser Ser Gly Leu Leu Val Gly Ala Asn Ile Met Met Asp Glu Asn		

450	455	460
Lys Asn Pro Asp Ala Gln Pro Ser Lys Leu Gly Thr Asn Ile Gln Arg		
465	470	475
480		
Val Ile Leu Val Leu Ser Asp Gly Glu Asp Asn Trp Pro Thr Tyr Ser		
485	490	495
Thr Leu Thr Thr Leu Leu Asn Asn Gly Met Cys Asp Lys Ile Arg Glu		
500	505	510
Gln Leu Gly Lys Leu Gln Asp Pro Asn Leu Arg Glu Leu Pro Gly Arg		
515	520	525
Ile Ala Phe Val Ala Phe Gly Tyr Ser Pro Pro Ala Asn Gln Val Ala		
530	535	540
Ala Trp Lys Lys Cys Val Gly Asp Gln Tyr Tyr Thr Ala Tyr Ser Lys		
545	550	555
560		
Glu Glu Leu Leu Asp Ser Phe Lys Gln Ile Ile Gly Phe Glu Glu Glu		
565	570	575
Val Gly Arg Ser Ser Ser His Lys Pro Lys Phe		
580	585	

<210> 60
<211> 5798
<212> DNA
<213> Pasteurella multocida

<220>
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<222> (698)..(1468)

<220>
<223> unknown D2

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ttattattat caggcctata ttatttatat gcagtaaaaa acgattcaaa ttttgcata 180
ggtttatcta ttatttttagt ttatttattat gtcattccag ggattttgac aaatgctatt 240
ttgaaagcta aggtgaaaaa aatcatggta gatttaccag gttttattga cttagttgca 300
gttaaatgttc aaacaggat tagtattgat gcggctttaa aacaagtggc aatcgatttt 360
aagaaaactta atccagatct tacttatgtg atgttaagga ttattagaaa atctgaactt 420
acgggattat cacaagcggt acaggatctt tcgatctcat tgccaacaac agaaataaga 480
atgtttgtta ctgttttaca acagagtta aattttggtt cttcaattta ttctcactta 540
attcagttgt ctgcagatat cagggagata caattattaa tcattgagga aaagtttaggt 600
acattatcag ctaaaatgag tatcccattg atttgttta ttatgttccc aataatcatt 660
ttaattctag caccaggtat aatgagggtta tttccaa atg ttt aaa ttt acc 715

	Met	Phe	Phe	Lys	Phe	Thr	
	1					5	
aag aaa atc gtt ttt gtt agt tta gct tta tct gtc gtt ggt tgt tct							763
Lys Lys Ile Val Phe Val Ser Leu Ala Leu Ser Val Val Gly Cys Ser							
10	15			20			
acc cat tct cag caa ggc atg aca cag aaa agt atg tca tct gaa aca							811
Thr His Ser Gln Gln Gly Met Thr Gln Lys Ser Met Ser Ser Glu Thr							
25	30			35			
ata acg gca aaa gag act tta tat gaa agt acg caa aat tat tcg gca							859
Ile Thr Ala Lys Glu Thr Leu Tyr Glu Ser Thr Gln Asn Tyr Ser Ala							
40	45			50			
ctc att tca ctg tat cgc gat gtg ttg aaa gcc aaa gaa gat cct tca							907
Leu Ile Ser Leu Tyr Arg Asp Val Leu Lys Ala Lys Glu Asp Pro Ser							
55	60			65			70
ata cgc tat aaa tta gcg aag aca tac tat cag cga ggt gac agc aaa							955
Ile Arg Tyr Lys Leu Ala Lys Thr Tyr Tyr Gln Arg Gly Asp Ser Lys							
75	80			85			
tct tct tta ctt tat tta acg cca tta ctg aat gat aat acg aag ctt							1003
Ser Ser Leu Leu Tyr Leu Thr Pro Leu Leu Asn Asp Asn Thr Lys Leu							
90	95			100			
gct aca caa gcg aaa ata tta cag ata aaa aat cta att caa tta aat							1051
Ala Thr Gln Ala Lys Ile Leu Gln Ile Lys Asn Leu Ile Gln Leu Asn							
105	110			115			
aat ttc caa gaa gca att tct gtc gca aat gaa ctc tta tta aaa tca							1099
Asn Phe Gln Glu Ala Ile Ser Val Ala Asn Glu Leu Leu Leu Lys Ser							
120	125			130			
cct aat gaa gga gaa gta tat aat tta aga ggt atc gct tat gcg caa							1147
Pro Asn Glu Gly Glu Val Tyr Asn Leu Arg Gly Ile Ala Tyr Ala Gln							
135	140			145			150
aat ggg aat ttg gtg aat gcc cga aat gat atc aat aaa gca aga gag							1195
Asn Gly Asn Leu Val Asn Ala Arg Asn Asp Ile Asn Lys Ala Arg Glu							
155	160			165			
ttc ttt att aat gat aat gtt gct att aat aat tta gcc atg cta aat							1243
Phe Phe Ile Asn Asp Asn Val Ala Ile Asn Asn Leu Ala Met Leu Asn							
170	175			180			
att att aat ggc gat ttt aat aat gct gtt tct tta ctg ttg cca caa							1291
Ile Ile Asn Gly Asp Phe Asn Asn Ala Val Ser Leu Leu Leu Pro Gln							
185	190			195			
tat tta aat ggc gtt aag aat tct cga ttg att cat aat ctt gtt ttt							1339
Tyr Leu Asn Gly Val Lys Asn Ser Arg Leu Ile His Asn Leu Val Phe							
200	205			210			
gct tta gtt aaa aat ggt gat ctt gat tat gca aaa gat atc att gtt							1387
Ala Leu Val Lys Asn Gly Asp Leu Asp Tyr Ala Lys Asp Ile Ile Val							
215	220			225			230
aaa gag cgt tta aat act tca cca gat gat tta att aat gca ttg aaa							1435
Lys Glu Arg Leu Asn Thr Ser Pro Asp Asp Leu Ile Asn Ala Leu Lys							
235	240			245			

aaa act aca cat gta tca aaa ggt gta act cg_g taacactaag gatttgat_t 1488
Lys Thr Thr His Val Ser Lys Gly Val Thr Arg
250 255

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gttctattt tttgttgtga tg_{ttt}tattt tgaattttgt cgattagcgg ttgcgacagc 1608
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<210> 61

<211> 257

<212> PRT

<213> Pasteurella multocida

<400> 61

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Ser Val Val Gly Cys Ser Thr His Ser Gln Gln Gly Met Thr Gln Lys
20 25 30

Ser Met Ser Ser Glu Thr Ile Thr Ala Lys Glu Thr Leu Tyr Glu Ser
35 40 45

Thr Gln Asn Tyr Ser Ala Leu Ile Ser Leu Tyr Arg Asp Val Leu Lys
50 55 60

Ala Lys Glu Asp Pro Ser Ile Arg Tyr Lys Leu Ala Lys Thr Tyr Tyr
65 70 75 80

Gln Arg Gly Asp Ser Lys Ser Ser Leu Leu Tyr Leu Thr Pro Leu Leu
85 90 95

Asn Asp Asn Thr Lys Leu Ala Thr Gln Ala Lys Ile Leu Gln Ile Lys
100 105 110

Asn Leu Ile Gln Leu Asn Asn Phe Gln Glu Ala Ile Ser Val Ala Asn
115 120 125

Glu Leu Leu Leu Lys Ser Pro Asn Glu Gly Glu Val Tyr Asn Leu Arg
130 135 140

Gly Ile Ala Tyr Ala Gln Asn Gly Asn Leu Val Asn Ala Arg Asn Asp
145 150 155 160

Ile Asn Lys Ala Arg Glu Phe Phe Ile Asn Asp Asn Val Ala Ile Asn
165 170 175

Asn Leu Ala Met Leu Asn Ile Ile Asn Gly Asp Phe Asn Asn Ala Val
180 185 190

Ser Leu Leu Leu Pro Gln Tyr Leu Asn Gly Val Lys Asn Ser Arg Leu
195 200 205

Ile His Asn Leu Val Phe Ala Leu Val Lys Asn Gly Asp Leu Asp Tyr
210 215 220

Ala Lys Asp Ile Ile Val Lys Glu Arg Leu Asn Thr Ser Pro Asp Asp
225 230 235 240

Leu Ile Asn Ala Leu Lys Lys Thr Thr His Val Ser Lys Gly Val Thr
245 250 255

Arg

<210> 62

<211> 1788

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (1)..(600)

<220>

<223> unknown K

<400> 62

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aaa gat gac acc agt ttt gtg act gaa gga aat aac ttt atc aca gca 96
Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala
20 25 30

aaa gac aac tta gaa atc acg gca aaa aat gtt caa att gat caa gcg 144
Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala
35 40 45

aaa aat att caa tta aac gcg aat atc acg atc aat acc aag tct ggt 192
Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly
50 55 60

ttt gtg aat tac ggt acc tta gca agt gct caa aat tta acg att aat 240
Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn
65 70 75 80

acc gaa caa ggc agc att tat aac ata ggc ggt atc ttg ggg gcg ggt 288
Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly
85 90 95

aaa agt ttg aat ctg agc gcg aaa aga gga gaa aac caa gga gga tat 336
Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr
100 105 110

ctt att aat caa ggt aag agt cta ctc cat tct gaa ggc gcc atg aac 384
Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn
115 120 125

ctc aca gcg gat cgc acg gtg tac aat tta ggg aat att ttt gct aaa 432
Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys

<210> 63
<211> 200
<212> PRT
<213> Pasteurella multocida

<400> 63
Val Asn Thr Gly Leu Ile His Ser Asn Gly Asn Ala Lys Leu Thr Phe
1 5 10 15
Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala
20 25 30
Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala
35 40 45
Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly
50 55 60
Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn
65 70 75 80
Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly
85 90 95
Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr
100 105 110
Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn
115 120 125
Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys
130 135 140
Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu
145 150 155 160
Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr
165 170 175
Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr
180 185 190
Glu Leu Asn Val Asp Arg Val Ser
195 200

<210> 64
<211> 278
<212> DNA
<213> *Pasteurella multocida*

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<222> (108) .. (278)

<220>
<223> unknown O

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cattacccaa atggaaataa accttaacca tagcaagaga gaagaaa atg aaa att 116
Met Lys Ile
1
act att aca cga aat cat cca gaa gta ttt caa gaa tcc gct cgt tta 164
Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser Ala Arg Leu
5 10 15

gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca tta aca ttg 212
Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala Leu Thr Leu
20 25 30 35
gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt gag gag gaa 260
Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly Glu Glu
40 45 50
agc aaa agg gga cat agt 278
Ser Lys Arg Gly His Ser
55

<210> 65
<211> 57
<212> PRT
<213> Pasteurella multocida

<400> 65
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Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
20 25 30
Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
35 40 45
Glu Glu Glu Ser Lys Arg Gly His Ser
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<210> 66
<211> 1020
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1)..(597)

<220>
<223> unknown P

<400> 66 48
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1 5 10 15
gca atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att 96
Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile
20 25 30
tca aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat 144
Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr
35 40 45
ttt gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa 192
Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln
50 55 60
ggc atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta 240
Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu

65	70	75	80	
cgc acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc				288
Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg				
85	90	95		
act gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca				336
Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala				
100	105	110		
gtg gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca				384
Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala				
115	120	125		
atc aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc				432
Ile Asn Ala Lys Trp Arg Asp Tyr Thr Lys Gly Tyr Leu Ile Gly				
130	135	140		
ggt aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa				480
Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys				
145	150	155	160	
gat gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc				528
Asp Ala Lys Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu				
165	170	175		
gaa cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat				576
Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp				
180	185	190		
ttt tca aat cgt tta gca tcg taagggtag aaaaatggctt taccacgcaa				627
Phe Ser Asn Arg Leu Ala Ser				
195				
acttaaattt atgaattttaa tcatcgacgg taacaaatat ctcggcgaag tcacggaagt				687
gactcaacca aaatttagcaa tgaaaatcga agaatttcgc gcgggcggta tgattggttc				747
ggatgttc aatctcgcc ttgaaaagct cgaagcggaa tttaaagccg gtggctacat				807
ggtcgaatta attaaaaat tcggcgggtc aatcaacggc attccattgc gttttcttgg				867
ctcatatcag cgtgatgaca cagaagaagt cacatctgtt gagcttgta tgcaaggctg				927
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Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile				
20 25 30				
Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr				
35 40 45				

Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln
50 55 60

Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu
65 70 75 80

Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg
85 90 95

Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala
100 105 110

Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala
115 120 125

Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly
130 135 140

Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys
145 150 155 160

Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu
165 170 175

Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp
180 185 190

Phe Ser Asn Arg Leu Ala Ser
195

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cgcgatggtc ttttgggtct ttatttacgt gctgttagc agtattgtgg catttaaaat 180
cggtcgcccg ttaattcagc tcaattttgc caatgaacgc ttaaacgcca actaccgtt 240
ttcacttatac cgtctgaaag aatatgctga aagcattgct ttttacgtg gtgaaaaaat 300
ggaaaaaacgt ctattgacca cacaatttaa tcaggtgatt gataacgttt ggcaagtaat 360
ctaccgcacc ttgaaattat ccggttttaa cttaatcatt acgcagattt cggtggttt 420
tccgctggtg attcaagtga cacgttattt tcgtcgacaa taggtgcata tgagggtgtt 480
agaatagcga tactttctgt tggaaaagta aactctttaa tataaataga aatcgcttga 540
atgattctcg ggcaaaaaat aatgtactca tttgcgatct catactgata atggcgaagt 600

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Met Ser Thr Tyr Phe Asp Lys Ile Glu Lys
1 5 10
gta aat tat gaa ggt gta act tca tct aat ccg ttt gca tat aag cat 1119
Val Asn Tyr Glu Gly Val Thr Ser Ser Asn Pro Phe Ala Tyr Lys His
15 20 25
tat gat gct aat caa gtt att tta ggt aag acg atg gct gaa cac tta 1167
Tyr Asp Ala Asn Gln Val Ile Leu Gly Lys Thr Met Ala Glu His Leu
30 35 40
cgt tta gcc gtc tgg ttt tgg cac act ttc tgg tgg aca ggg aat gat 1215
Arg Leu Ala Val Cys Tyr Trp His Thr Phe Cys Trp Thr Gly Asn Asp
45 50 55
atg ttc ggt gtc ggt tct ttc gat cgt tgg cag aag gcg agt gat 1263
Met Phe Gly Val Gly Ser Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp
60 65 70
tca tta gca ggt gca aaa caa aaa gca gat atc gct ttt gaa ttt ttc 1311
Ser Leu Ala Gly Ala Lys Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe
75 80 85 90
agt aaa tta ggc ata cct tat tat tgg ttt cat gat gtt gat gtt gcg 1359
Ser Lys Leu Gly Ile Pro Tyr Tyr Cys Phe His Asp Val Asp Val Ala
95 100 105
cca gaa ggt cat tca ttt aaa gaa tat ttg tcg aac ttt aat aca atg 1407
Pro Glu Gly His Ser Phe Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met
110 115 120
atc gat gtt tta gcg cag aaa caa gaa gaa aca ggc gtc aaa ttg ttg 1455
Ile Asp Val Leu Ala Gln Lys Gln Glu Thr Gly Val Lys Leu Leu
125 130 135
tgg ggg act gca aat tgg ttt aca cac cct cgt tat atg tct ggt gct 1503
Trp Gly Thr Ala Asn Cys Phe Thr His Pro Arg Tyr Met Ser Gly Ala
140 145 150
gca aca aat ccg aat cca gaa att ttt gct tgg gct gct gca caa gta 1551
Ala Thr Asn Pro Asn Pro Glu Ile Phe Ala Trp Ala Ala Gln Val
155 160 165 170
ttt act gcc atg ggg gca act cag cgt tta ggt ggt gaa aat tat gtt 1599
Phe Thr Ala Met Gly Ala Thr Gln Arg Leu Gly Glu Asn Tyr Val
175 180 185
ttg tgg gga gga cgt gaa gga tat gaa acg tta tta aat acc aat tta 1647

Leu Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu
190 195 200

aaa cag gag cga gag caa att gga cgt ttc atg caa atg gtg gtt gag 1695
Lys Gln Glu Arg Glu Gln Ile Gly Arg Phe Met Gln Met Val Val Glu
205 210 215

cat aaa tat aaa atc ggt ttt aac ggg act ttg ctg att gaa cca aag 1743
His Lys Tyr Lys Ile Gly Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys
220 225 230

cca caa gag cca acg aaa cat caa tat gac tat gat gtg gcg acc gtt 1791
Pro Gln Glu Pro Thr Lys His Gln Tyr Asp Tyr Asp Val Ala Thr Val
235 240 245 250

tat ggc ttt tta aag cag ttt ggt tta gaa aaa gaa att aaa gtg aat 1839
Tyr Gly Phe Leu Lys Gln Phe Gly Leu Glu Lys Glu Ile Lys Val Asn
255 260 265

att gaa gct aat cac gca aca tta gct gga cac act ttc cag cat gaa 1887
Ile Glu Ala Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu
270 275 280

gtc gcc atg gct aca gcg tta gat att ttt ggt tct att gat gca aat 1935
Val Ala Met Ala Thr Ala Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn
285 290 295

cgt ggt gat cca caa tta ggt tgg gat acc gat caa ttc cct aat agc 1983
Arg Gly Asp Pro Gln Leu Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser
300 305 310

gta gaa gaa aat act ttg gtc ata tat gaa att ctc aaa gca ggg ggc 2031
Val Glu Glu Asn Thr Leu Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly
315 320 325 330

ttt aca acc ggt ggt ttt aat ttt gat gct aaa atc cgt cgg cag agt 2079
Phe Thr Thr Gly Phe Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser
335 340 345

acg gat cct tac gat tta ttt cat gga cat att ggc gcg att gat gta 2127
Thr Asp Pro Tyr Asp Leu Phe His Gly His Ile Gly Ala Ile Asp Val
350 355 360

ctt gcc tta tca cta aaa tgt gcg gcg aaa atg ctt gaa gag caa gct 2175
Leu Ala Leu Ser Leu Lys Cys Ala Ala Lys Met Leu Glu Glu Gln Ala
365 370 375

tta caa aaa gtc gtc aat caa cgt tat gct ggt tgg aca tca tca ctt 2223
Leu Gln Lys Val Val Asn Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu
380 385 390

ggt caa ctt gtt caa atc cgg tcc tac cac gcg tgt ctg caa tac aga 2271
Gly Gln Leu Val Gln Ile Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg
395 400 405 410

cta aca aaa gtg ctt taaaacgttc cggcttacgc cagacatcta gacgattgaa 2326
Leu Thr Lys Val Leu
415

taatttcaat attgtctccg cacgtaattc aaaggctttg tgtatgtgcg aatgatattc 2386

acaacaaagt tctgcaaaat cttgaattgc gtgaggtaat ttaaagcgct gacataagcg 2446

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20 25 30
Ile Leu Gly Lys Thr Met Ala Glu His Leu Arg Leu Ala Val Cys Tyr
35 40 45
Trp His Thr Phe Cys Trp Thr Gly Asn Asp Met Phe Gly Val Gly Ser
50 55 60
Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp Ser Leu Ala Gly Ala Lys
65 70 75 80
Gln Lys Ala Asp Ile Ala Phe Glu Phe Ser Lys Leu Gly Ile Pro
85 90 95
Tyr Tyr Cys Phe His Asp Val Asp Val Ala Pro Glu Gly His Ser Phe
100 105 110
Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met Ile Asp Val Leu Ala Gln
115 120 125
Lys Gln Glu Glu Thr Gly Val Lys Leu Leu Trp Gly Thr Ala Asn Cys
130 135 140
Phe Thr His Pro Arg Tyr Met Ser Gly Ala Ala Thr Asn Pro Asn Pro
145 150 155 160
Glu Ile Phe Ala Trp Ala Ala Gln Val Phe Thr Ala Met Gly Ala
165 170 175
Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val Leu Trp Gly Gly Arg Glu
180 185 190
Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu Lys Gln Glu Arg Glu Gln
195 200 205
Ile Gly Arg Phe Met Gln Met Val Val Glu His Lys Tyr Lys Ile Gly
210 215 220
Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys Pro Gln Glu Pro Thr Lys
225 230 235 240
His Gln Tyr Asp Tyr Asp Val Ala Thr Val Tyr Gly Phe Leu Lys Gln
245 250 255
Phe Gly Leu Glu Lys Glu Ile Lys Val Asn Ile Glu Ala Asn His Ala
260 265 270

Thr Leu Ala Gly His Thr Phe Gln His Glu Val Ala Met Ala Thr Ala
275 280 285

Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn Arg Gly Asp Pro Gln Leu
290 295 300

Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser Val Glu Glu Asn Thr Leu
305 310 315 320

Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly Phe Thr Thr Gly Gly Phe
325 330 335

Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser Thr Asp Pro Tyr Asp Leu
340 345 350

Phe His Gly His Ile Gly Ala Ile Asp Val Leu Ala Leu Ser Leu Lys
355 360 365

Cys Ala Ala Lys Met Leu Glu Glu Gln Ala Leu Gln Lys Val Val Asn
370 375 380

Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu Gly Gln Leu Val Gln Ile
385 390 395 400

Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg Leu Thr Lys Val Leu
405 410 415

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<222> (298)..(1905)

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gtcaagaata atgtgatgtt accggtgatt aataccaata ttgaaccgca ctttgatgcc 180

cttagagcca cccaaatgaa cacgaaagtg ctcgataacct caaaagtgaa tgccgaacaa 240

gtcaaaaaat ggattgctgt ttggcaaacg accctaacc aataattgtt tgtcttg 297

atg ttt aag cga ttt cgt gca ttc aca tac cgt ccc gcc agt tat ctt 345
Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu
1 5 10 15

ggc ggg atg ttg gtg att gtt ttt ctg agc gct ttt tat gcg ttc gcc 393
Gly Gly Met Leu Val Ile Val Phe Leu Ser Ala Phe Tyr Ala Phe Ala
20 25 30

tta ggg gcg gtt ttt tcg ctc cct ttt gcg cgc agt tgg aca gcg ttg 441
Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Thr Ala Leu
35 40 45

ttg	agt	gat	cag	tat	tta	caa	cac	gtg	atc	atc	ttt	agc	ttt	tgg	caa	489	
Leu	Ser	Asp	Gln	Tyr	Leu	Gln	His	Val	Ile	Ile	Phe	Ser	Phe	Trp	Gln		
50					55						60						
gcc	ttt	ctg	tcg	gcg	gta	ctt	gcg	gtc	ctc	ttt	ggt	ggc	att	gta	gca	537	
Ala	Phe	Leu	Ser	Ala	Val	Leu	Ala	Val	Leu	Phe	Gly	Gly	Ile	Val	Ala		
65					70					75				80			
cga	gcc	ttt	ttt	tat	caa	ccg	ttt	gtg	ggc	aag	aaa	ctg	atc	ctc	aaa	585	
Arg	Ala	Phe	Phe	Tyr	Gln	Pro	Phe	Val	Gly	Lys	Lys	Lys	Leu	Ile	Leu	Lys	
85								90				95					
tta	ttt	tca	ctg	act	ttt	gtg	tta	cct	gcc	tta	gtg	gct	att	ttt	ggt	633	
Leu	Phe	Ser	Leu	Thr	Phe	Val	Leu	Pro	Ala	Leu	Val	Ala	Ile	Phe	Gly		
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Leu	Leu	Gly	Val	Tyr	Gly	Ala	Ser	Gly	Trp	Leu	Ala	Met	Leu	Ser	Gln		
115							120					125					
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Phe	Phe	Ala	Trp	Asp	Trp	Thr	Pro	Asn	Ile	Tyr	Gly	Leu	Thr	Gly	Ile		
130							135				140						
tta	ctg	gct	cat	ctt	ttt	aat	gtc	cca	tta	gct	tgt	cgc	ctg	ttt		777	
Leu	Leu	Ala	His	Leu	Phe	Phe	Asn	Val	Pro	Leu	Ala	Cys	Arg	Leu	Phe		
145							150				155			160			
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Leu	Gln	Gly	Leu	Gln	Ala	Ile	Pro	Val	Gln	Gln	Arg	Gln	Leu	Ala	Ala		
165							170				175						
caa	ctc	aat	tta	cgt	ggt	tgg	cat	ttt	ata	cgt	ctg	att	gag	tgg	ccc	873	
Gln	Leu	Asn	Leu	Arg	Gly	Trp	His	Phe	Ile	Arg	Leu	Ile	Glu	Trp	Pro		
180							185				190						
tat	tta	cgc	cag	caa	ttg	tta	cct	gca	ttt	act	ttg	att	ttc	atg	ctg	921	
Tyr	Leu	Arg	Gln	Gln	Leu	Leu	Leu	Pro	Ala	Phe	Thr	Leu	Ile	Phe	Met	Leu	
195							200				205						
tgt	ttt	acc	agt	ttt	gct	att	gtg	ctc	act	tta	ggt	ggc	gga	ccg	aaa	969	
Cys	Phe	Thr	Ser	Phe	Ala	Ile	Val	Leu	Thr	Leu	Gly	Gly	Gly	Pro	Lys		
210							215				220						
tat	acc	acg	ttg	gaa	gtg	gct	atc	tat	caa	gct	att	tta	ttt	gag	ttt	1017	
Tyr	Thr	Thr	Leu	Glu	Val	Ala	Ile	Tyr	Gln	Ala	Ile	Leu	Phe	Glu	Phe		
225							230				235			240			
gat	gta	ccg	aaa	gcc	ggc	tta	ttt	gct	tta	tta	caa	ttt	gtt	ttt	tgt	1065	
Asp	Val	Pro	Lys	Ala	Gly	Leu	Phe	Ala	Leu	Leu	Gln	Phe	Val	Phe	Cys		
245							250				255						
ttt	ctg	tta	tcc	acg	ctg	agt	agc	ttt	ttt	tct	cca	gcc	ccc	gcc	acg	1113	
Phe	Leu	Leu	Phe	Thr	Leu	Ser	Ser	Phe	Phe	Ser	Pro	Ala	Pro	Ala	Thr		
260							265				270						
aca	tta	cac	agt	caa	cct	act	tgg	ttt	gct	ccc	caa	tgc	tat	tgg	gtt	1161	
Thr	Leu	His	Ser	Gln	Pro	Thr	Trp	Phe	Ala	Pro	Gln	Ser	Tyr	Trp	Val		
275							280				285						
aaa	tta	tgg	caa	cgt	atg	atc	att	gtg	tgt	gct	aca	gta	ttt	atc	tta	1209	
Lys	Leu	Trp	Gln	Arg	Met	Ile	Ile	Val	Cys	Ala	Thr	Val	Phe	Ile	Leu		
290							295				300						

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Leu Pro Leu Leu Asn Thr Leu Val Ser Ala Leu Leu Ser Ser Gln Phe	
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Phe Thr Leu Trp Leu Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser	
325 330 335	
ctc acc atc gcc ccc act tct gca ttg ctc gct tta gta ctg tct ttt	1353
Leu Thr Ile Ala Pro Thr Ser Ala Leu Leu Ala Leu Val Leu Ser Phe	
340 345 350	
gcc tta tta ttg ctt gcc aga gaa tta cat tgg cga cat tat cgc agc	1401
Ala Leu Leu Leu Ala Arg Glu Leu His Trp Arg His Tyr Arg Ser	
355 360 365	
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Leu Ser His Val Ile Leu Asn Ile Gly Ala Thr Ile Leu Ala Ile Pro	
370 375 380	
acg tta gtg tta gct att ggt tta ttc att tta tta cgt gag atc gat	1497
Thr Leu Val Leu Ala Ile Gly Leu Phe Ile Leu Leu Arg Glu Ile Asp	
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Phe Ser Pro Tyr His Leu Phe Gly Val Val Val Cys Cys Asn Ala Leu	
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Ala Ala Met Pro Phe Val Leu Arg Ile Leu Ala Leu Pro Met His Asn	
420 425 430	
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Asn Met Ile Tyr Tyr Glu Lys Leu Cys Gln Ser Leu Asn Leu Arg Gly	
435 440 445	
tgg caa cgt ttt cga ttg att gaa tgg cac aag ctt cgt gcg cca atg	1689
Trp Gln Arg Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met	
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Lys Tyr Ala Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr	
465 470 475 480	
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Ala Ile Ala Leu Phe Gly Gln Ala Asp Phe Thr Ser Leu Pro His Leu	
485 490 495	
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Leu Tyr Gln Gln Leu Gly His Tyr Arg Ser Gln Glu Ala Ala Val Thr	
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gcg ttt att tta ttg gtt ttt tgt ttg agt gtt ttt atg att att gaa	1881
Ala Phe Ile Leu Leu Val Phe Cys Leu Ser Val Phe Met Ile Ile Glu	
515 520 525	
cga cat cag gaa ccg cgt gat gat taatttaaac ggtgttcagt tttcctataa	1935
Arg His Gln Glu Pro Arg Asp Asp	
530 535	
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cgccagtggc gcagggaga gtagcattttt aaatttgatt gcgggttttg cattgccaca	2055

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aattatccac tttaatgtcg attaaaacgg gggatgtcc agaggattgt ggctactgtc 2835
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ttgttggaaa agccaaaatt gccaaagcac gtggtgcagg gcgctttgt atgggggctg 2955
catggcgtgg accgaaaccg aaagacattt aaaaagttac cgcaatcatt aaagcgggtga 3015
aagaactggg cttagaaacc tgggttacct ttgtttatt gcaagatggg atggcagaag 3075
atttaaaaga agcgggttt gattattata accataatct cgatacagcc ccagaacact 3135
acggtaatgt gattggtacc cgtcaattt atgatcgat taatacgta ggtaaagtgc 3195
gttaagctgg cttaaaagtg tgctgtggcg ggattattgg catgaatgaa acccgtaaag 3255
aaagagcagg attaattgct agcttagcta atttagaccc gcaacccgaa tcggtgccga 3315
ttaatcaatt agtggaaagtg gaaggtaccc ctttagccga tgcggcagaa ttagactgga 3375
cagaatttgt gcgcaattt gcggtggcg gtattaccat gccgaaaagc tatgtacgtt 3435
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cgaatt 3501

<210> 71
<211> 536
<212> PRT
<213> Pasteurella multocida

<400> 71
Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu
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Gly Gly Met Leu Val Ile Val Phe Leu Ser Ala Phe Tyr Ala Phe Ala
20 25 30

Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Thr Ala Leu
35 40 45

Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln
50 55 60

Ala Phe Leu Ser Ala Val Leu Ala Val Leu Phe Gly Gly Ile Val Ala
65 70 75 80

Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys
85 90 95

Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly
100 105 110

Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln
115 120 125

Phe Phe Ala Trp Asp Trp Thr Pro Asn Ile Tyr Gly Leu Thr Gly Ile
130 135 140

Leu Leu Ala His Leu Phe Phe Asn Val Pro Leu Ala Cys Arg Leu Phe
145 150 155 160

Leu Gln Gly Leu Gln Ala Ile Pro Val Gln Gln Arg Gln Leu Ala Ala
165 170 175

Gln Leu Asn Leu Arg Gly Trp His Phe Ile Arg Leu Ile Glu Trp Pro
180 185 190

Tyr Leu Arg Gln Leu Leu Pro Ala Phe Thr Leu Ile Phe Met Leu
195 200 205

Cys Phe Thr Ser Phe Ala Ile Val Leu Thr Leu Gly Gly Pro Lys
210 215 220

Tyr Thr Thr Leu Glu Val Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe
225 230 235 240

Asp Val Pro Lys Ala Gly Leu Phe Ala Leu Leu Gln Phe Val Phe Cys
245 250 255

Phe Leu Leu Phe Thr Leu Ser Ser Phe Phe Ser Pro Ala Pro Ala Thr
260 265 270

Thr Leu His Ser Gln Pro Thr Trp Phe Ala Pro Gln Ser Tyr Trp Val
275 280 285

Lys Leu Trp Gln Arg Met Ile Ile Val Cys Ala Thr Val Phe Ile Leu
290 295 300

Leu Pro Leu Leu Asn Thr Leu Val Ser Ala Leu Leu Ser Ser Gln Phe
305 310 315 320

Phe Thr Leu Trp Leu Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser
325 330 335

Leu Thr Ile Ala Pro Thr Ser Ala Leu Leu Ala Leu Val Leu Ser Phe
340 345 350

Ala Leu Leu Leu Leu Ala Arg Glu Leu His Trp Arg His Tyr Arg Ser
355 360 365

Leu Ser His Val Ile Leu Asn Ile Gly Ala Thr Ile Leu Ala Ile Pro
370 375 380

Thr Leu Val Leu Ala Ile Gly Leu Phe Ile Leu Leu Arg Glu Ile Asp
385 390 395 400

Phe Ser Pro Tyr His Leu Phe Gly Val Val Val Cys Cys Asn Ala Leu
405 410 415

Ala Ala Met Pro Phe Val Leu Arg Ile Leu Ala Leu Pro Met His Asn
420 425 430

Asn Met Ile Tyr Tyr Glu Lys Leu Cys Gln Ser Leu Asn Leu Arg Gly
435 440 445

Trp Gln Arg Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met
450 455 460

Lys Tyr Ala Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr
465 470 475 480

Ala Ile Ala Leu Phe Gly Gln Ala Asp Phe Thr Ser Leu Pro His Leu
485 490 495

Leu Tyr Gln Gln Leu Gly His Tyr Arg Ser Gln Glu Ala Ala Val Thr
500 505 510

Ala Phe Ile Leu Leu Val Phe Cys Leu Ser Val Phe Met Ile Ile Glu
515 520 525

Arg His Gln Glu Pro Arg Asp Asp
530 535

<210> 72
<211> 3182
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1544)...(2809)

<220>
<223> ygiK

<400> 72
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tgcaggagaa aaagtttatg aaatccaaaa agaatggact gacaatattg aaaaagcttc 180
caatggaga ataagtatac agtttattacc tctcgactca gtcttaaat ctagtgacat 240
gctttctggt gttcgaaata aaatttattga tggagcgggtt gcaacagcgg caatgtatgc 300
aggcactgac cctggattcg gattaattgg tgatactatt tctgcttgaa accatgacga 360
agatatttta aattttact ataatggagg tggtttgaa gttgttgata atattttcca 420
acaatatggt gccaaactca ttgggtgtatc anttacggga gcagaatcat taccatcgaa 480

agtaaaaata gctaatactg aagattttaa aggtataaaa attcgggctc cctctggtcc 540
tatccaaaaa ttgttgcaa gattaggagc cgctcctgtt ggtcttcctg gttcagaaat 600
ctatactagt tttagaaaaag gtattattga tgctgccat ttctcaacgt ttgcaaataa 660
tcaaggacaaa ggagtccatg atattgcaaa atatccaatc tatccggaa ttcattttc 720
accagccgtt catatgatta tgaatcataa aacttggagt agcttaactc catcgatca 780
agcattctt attgcttact ttaaaggat ggctctcgat actctgactc gtgctcatta 840
tgaagataaa ctagcatata aagaagcact tgagaaagga gtacaaccag tttcttggaa 900
tcaacaagaa attacaaaag ttcgttctat cgctaaagaa atttggcaag agatagctca 960
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gaatgctgca ataatcgta agatggataa gacgatatcg tcttatccat taaggagtaa 1080
aacatgctt tttctaaata tttattatgg ctctgtataa agctagatca aatattcatt 1140
aaagtaggtt attacgttcc ttatattttt ctattagttt ttatcattgg ttttacgagg 1200
ttgttgctcg gtatttattc tctagccaa cactttgggt tcatgaagta acaacattt 1260
taataagtct atcattactt tatggtgag tagcttgtaa cgccagtaat aaacatattg 1320
ccatgacatt tattagacaa aaattaccta ataagatcaa atggttacta gaactcttag 1380
ttgaaatact tatttttattc ttctttattt tgcttagtta cggagcatac ttatcagcta 1440
gagaagcatt atttactcca tcaggaaaat tcaaaatgca aacttctgga agtgtattag 1500
acatgccatt tccagcaatt gaaaaaagtt tcttctttat ttc atg cct cat cat 1555
Met Pro His His
1
tgt tgc tct ttc agt act aca tat att ccg tca cat cta tac aaa ata 1603
Cys Cys Ser Phe Ser Thr Thr Tyr Ile Pro Ser His Leu Tyr Lys Ile
5 10 15 20
tca gga gga att atc atc agt ata agt gca ttt ggg ata ggt att gga act 1651
Ser Gly Gly Ile Ile Met Ile Ser Ala Phe Gly Ile Gly Ile Gly Thr
25 30 35
ctt att atc ttt tta atg atg att tcc ctt tta ttt att gga atg cca 1699
Leu Ile Ile Phe Leu Met Met Ile Ser Leu Leu Phe Ile Gly Met Pro
40 45 50
tta ggt ttt ctc act ggg tta atc gct tta gtt att tca tat ctt tgg 1747
Leu Gly Phe Leu Thr Gly Leu Ile Ala Leu Val Ile Ser Tyr Leu Trp
55 60 65
ttt gat act acc gca ata atg caa atg ata gct tca cgt gtc act gat 1795
Phe Asp Thr Thr Ala Ile Met Gln Met Ile Ala Ser Arg Val Thr Asp
70 75 80
ttc aca tca tct tac act ttt gta gct gtg cct atg ttt gtt ctt atg 1843
Phe Thr Ser Ser Tyr Thr Phe Val Ala Val Pro Met Phe Val Leu Met
85 90 95 100
gca aca tta ctt gat aag act gga att gct aga gat ctc tac aac gca 1891

Ala Thr Leu Leu Asp Lys Thr Gly Ile Ala Arg Asp Leu Tyr Asn Ala	105	110	115	
atg cga gtc att ggc ggt cga tta cga ggt gga att gca att caa tcg				1939
Met Arg Val Ile Gly Gly Arg Leu Arg Gly Gly Ile Ala Ile Gln Ser	120	125	130	
atg ttt gtt gca gtt cta ctt gct acg atg tca ggt att atc ggt gga				1987
Met Phe Val Ala Val Leu Leu Ala Thr Met Ser Gly Ile Ile Gly Gly	135	140	145	
gaa act gtt tta tta ggc atg ttg gca tta cca caa atg tta cgc tta				2035
Glu Thr Val Leu Leu Gly Met Leu Ala Leu Pro Gln Met Leu Arg Leu	150	155	160	
ggc tat aat aaa aac tta gct ata gga act gtt gta gca gga gga gca				2083
Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val Ala Gly Gly Ala	165	170	175	180
ttg ggt aca atg gtt cct cca agt atc gtg ttg att att tac gga atg				2131
Leu Gly Thr Met Val Pro Pro Ser Ile Val Leu Ile Ile Tyr Gly Met	185	190	195	
acc gca aat gtt tct att gga gaa cta ttt ctt gca gca att cca gcc				2179
Thr Ala Asn Val Ser Ile Gly Glu Leu Phe Leu Ala Ala Ile Pro Ala	200	205	210	
tcc tta cta ctt tct aca ttc tat att tta tat att cta gta ctt tgc				2227
Ser Leu Leu Leu Ser Thr Phe Tyr Ile Leu Tyr Ile Leu Val Leu Cys	215	220	225	
tac ttc aaa cct agc tat ggc cct gca atg cct agc tca gaa aat cat				2275
Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Pro Ser Ser Glu Asn His	230	235	240	
aca tta acg aaa gaa gat att aaa aaa att att cat gat att gca att				2323
Thr Leu Thr Lys Glu Asp Ile Lys Lys Ile Ile His Asp Ile Ala Ile	245	250	255	260
cca gta gct atc gcc aca tgg att tta gga agt att tat ggc ggg ata				2371
Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile Tyr Gly Gly Ile	265	270	275	
gca tca atc act gaa tct gcc tgt gtt ggt gta gtt ggg gta ata tta				2419
Ala Ser Ile Thr Glu Ser Ala Cys Val Gly Val Val Gly Val Ile Leu	280	285	290	
gca gca ttc tat cga aaa gaa tta aat ttc aaa ata gta caa gaa tca				2467
Ala Ala Phe Tyr Arg Lys Glu Leu Asn Phe Lys Ile Val Gln Glu Ser	295	300	305	
cta aaa cat aca atc aat act gtt ggt atg ata atc tgg gtc ggc att				2515
Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile Trp Val Gly Ile	310	315	320	
ggc gca aca atg att ata ggt att tat aat cta atg ggt ggg gac cga				2563
Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met Gly Gly Asp Arg	325	330	335	340
ttt ata gct aac tta ttc gct agc tta gat gcc tct cca att tat act				2611
Phe Ile Ala Asn Leu Phe Ala Ser Leu Asp Ala Ser Pro Ile Tyr Thr	345	350	355	

atc att att atg atg gtt att tta tta ata ctt ggt atg ttc tta gat	2659
Ile Ile Ile Met Met Val Ile Leu Leu Ile Leu Gly Met Phe Leu Asp	
360 365 370	
tgg att ggt gtt gcc atg ttg act ttc ctc aag aca agt aaa gcg aca	2707
Trp Ile Gly Val Ala Met Leu Thr Phe Leu Lys Thr Ser Lys Ala Thr	
375 380 385	
atc aat ttg tgt ttt gac ata gtc agg tac agt att tgg cgt ggt ccc	2755
Ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile Trp Arg Gly Pro	
390 395 400	
tcc ttc cac agt acc aat gtt cat cgt ggt acc ttt gtc ggg cgc ggt	2803
Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe Val Gly Arg Gly	
405 410 415 420	
act ttt tagtaaatct tgcgcgatac gaataaacgc attgatggca tttgctccgt	2859
Thr Phe	
tttgtggatc gactgccgca tgagcagatt tgccaaaaaa ttcaattaca tacttcccaa	2919
tccctttctt ttcgttaacg tttccactta gattgcccag aagccgatct gtctgaatgg	2979
gaacaagtgt tataccaaga agcgaatcca acaggtgaag tggtgatcgg tatggtgggt	3039
aaatacactg aattaccgga tgcctacaaa tcggttaatg aagcctgaa acacgcaggc	3099
ttaaaaaacc gtcttagcgt gcaaatcaa tatattgatt cacaagatgt ggaaacccaa	3159
ggcacagaag tgtagaagg cgt	3182

<210> 73
<211> 422
<212> PRT
<213> Pasteurella multocida

<400> 73	
Met Pro His His Cys Cys Ser Phe Ser Thr Thr Tyr Ile Pro Ser His	
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Leu Tyr Lys Ile Ser Gly Gly Ile Ile Met Ile Ser Ala Phe Gly Ile	
20 25 30	
Gly Ile Gly Thr Leu Ile Ile Phe Leu Met Met Ile Ser Leu Leu Phe	
35 40 45	
Ile Gly Met Pro Leu Gly Phe Leu Thr Gly Leu Ile Ala Leu Val Ile	
50 55 60	
Ser Tyr Leu Trp Phe Asp Thr Thr Ala Ile Met Gln Met Ile Ala Ser	
65 70 75 80	
Arg Val Thr Asp Phe Thr Ser Ser Tyr Thr Phe Val Ala Val Pro Met	
85 90 95	
Phe Val Leu Met Ala Thr Leu Leu Asp Lys Thr Gly Ile Ala Arg Asp	
100 105 110	
Leu Tyr Asn Ala Met Arg Val Ile Gly Gly Arg Leu Arg Gly Gly Ile	
115 120 125	
Ala Ile Gln Ser Met Phe Val Ala Val Leu Leu Ala Thr Met Ser Gly	

130	135	140
Ile Ile Gly Gly Glu Thr Val Leu Leu Gly Met Leu Ala Leu Pro Gln		
145	150	155
Met Leu Arg Leu Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val		
165	170	175
Ala Gly Gly Ala Leu Gly Thr Met Val Pro Pro Ser Ile Val Leu Ile		
180	185	190
Ile Tyr Gly Met Thr Ala Asn Val Ser Ile Gly Glu Leu Phe Leu Ala		
195	200	205
Ala Ile Pro Ala Ser Leu Leu Ser Thr Phe Tyr Ile Leu Tyr Ile		
210	215	220
Leu Val Leu Cys Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Pro Ser		
225	230	235
Ser Glu Asn His Thr Leu Thr Lys Glu Asp Ile Lys Lys Ile Ile His		
245	250	255
Asp Ile Ala Ile Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile		
260	265	270
Tyr Gly Gly Ile Ala Ser Ile Thr Glu Ser Ala Cys Val Gly Val Val		
275	280	285
Gly Val Ile Leu Ala Ala Phe Tyr Arg Lys Glu Leu Asn Phe Lys Ile		
290	295	300
Val Gln Glu Ser Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile		
305	310	315
Trp Val Gly Ile Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met		
325	330	335
Gly Gly Asp Arg Phe Ile Ala Asn Leu Phe Ala Ser Leu Asp Ala Ser		
340	345	350
Pro Ile Tyr Thr Ile Ile Ile Met Met Val Ile Leu Leu Ile Leu Gly		
355	360	365
Met Phe Leu Asp Trp Ile Gly Val Ala Met Leu Thr Phe Leu Lys Thr		
370	375	380
Ser Lys Ala Thr Ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile		
385	390	395
Trp Arg Gly Pro Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe		
405	410	415
Val Gly Arg Gly Thr Phe		
420		

<210> 74
<211> 2787
<212> DNA
<213> *Pasteurella multocida*

<220>

<221> CDS
<222> (463) .. (936)

<220>
<223> yhcJ

<400> 74
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gcatacaaag caagaatgtt ggccagtgtg tcatgcatcg cattggcagc atcagcttgt 120
ggcggtgcaa tctgttggcg ttgttctatt ttgccgtctg ttacaatagc cgaggcaatt 180
tttgttccac caatatctaa tgctaaacag cgcataaggct ctccttctgt gatgacttat 240
tttgcgatt tgacggcatc ggcaaaccag cttacgatat gttcgaggcg agtcagcgca 300
gatcctacgg tgacagagta agcaccaatc tcaattgcgg tttcgccaa ttctggggtg 360
ttatagcgcc cttctgccat cactcgccag ccagcagcat tcaaattttt gactaactga 420
taatccggtt cagctggaat ttcaccgcca gtataaccag ac atg gtg cta cca 474
Met Val Leu Pro
1
ata att tct acc cct aag ttg tgg caa tac atc cct tct tca aaa tta 522
Ile Ile Ser Thr Pro Lys Leu Trp Gln Tyr Ile Pro Ser Ser Lys Leu
5 10 15 20
gaa caa tcc gcc atg gct aaa caa cct aat tct ttg att cgt tta ata 570
Glu Gln Ser Ala Met Ala Lys Gln Pro Asn Ser Leu Ile Arg Leu Ile
25 30 35
atg gct tca cgt gta gtt gga cgg acg cga tcg gta cca tca aaa gca 618
Met Ala Ser Arg Val Val Gly Arg Thr Arg Ser Val Pro Ser Lys Ala
40 45 50
ata ata tcg gcg cct gct gcg gct aac tct tca atg tct tgc aaa aat 666
Ile Ile Ser Ala Pro Ala Ala Asn Ser Ser Met Ser Cys Lys Asn
55 60 65
ggg cta ata cga acg gga ctg tca ggt aaa tcg cgt tta acg ata cca 714
Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg Leu Thr Ile Pro
70 75 80
ata atc ggt aca ttg acg acg tta cgc gtg gct ttt aaa ttt tcg atc 762
Ile Ile Gly Thr Leu Thr Leu Arg Val Ala Phe Lys Phe Ser Ile
85 90 95 100
cct tca ata cgt aac ccg gca cca ccg ata acg gat gct tgc gcc 810
Pro Ser Ile Arg Asn Pro Ala Ala Pro Pro Ile Thr Asp Ala Cys Ala
105 110 115
atg gcg gca aca att tct ggc gag tcc att ggc cca tta tct acg ggc 858
Met Ala Ala Thr Ile Ser Gly Glu Ser Ile Gly Pro Leu Ser Thr Gly
120 125 130
tgg caa gat gcg att aag cca tat tta att tgt tct aaa act tgc gga 906
Trp Gln Asp Ala Ile Lys Pro Tyr Leu Ile Cys Ser Lys Thr Cys Gly
135 140 145
tgt gat agt ttt gac ata tta act cca gtc taaatttac aaaagaagat 956
Cys Asp Ser Phe Asp Ile Leu Thr Pro Val

150

155

tgactccaat ttgcataatgt taatcttata attaaaaaaat aacaacccaaa ataataaaaa 1016
ttttagatct ttgtcgata tttattcata gggaaatagac agcttaattt tagttatgtat 1076
ttgtcaatcc ttgttatattt ttgtgttgc tgggttgcga tacactgttc taatattgct 1136
ttgagcactt gataacccctt ctcattaaaa tgtaatccgt cggtacaaag gcgtaaatcc 1196
agttcaccgt tagaatcaca aaagtatttt tgggttcaa cgtaagtcac gtctgacgga 1256
caatgttgtt taaaataggt attgagccctg tgaatttgcg cgttagtgcg cgtattaatc 1316
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gaatgaccaa ttaagctgat attggcaggt ttggaaaatt ccgcatttt gctctgatag 1676
cggtgataaa tatttcgtatc acttagcatg tggacccctc tattttgaaa taaaacgcta 1736
agtattat aaaaacctgat atgcccgtt acagttaaact tatcttcgtt aggggtaaat 1796
attcaatttt gtgacgaacc tattttat gaaataaaac ttcattttct atataaaaaaa 1856
tagtttttc actttagaaat gccaacgtg tggaaattt ttcattcatca tttaacgta 1916
atcccaacgt aaccaataga ggagaactca taatgaaatt taaaaacta ctacttgcatt 1976
ctttatgtt aggtgttca gcttctgtat ttgcagcaga ttacgatctt aaattcggtt 2036
tgggtgcggg tccaagctca aacgaatata aagcagtaga attcttcgtt aaagaagtga 2096
aagaaaaatc caatggcaaa attgatgtgg ctattttccc tagtcacag ttaggtgtat 2156
accgtgtgat gattaaacaa taaaagacg gtgcatttgc cttaacgtt ggtgaatcag 2216
cacgtttcca aatttacttc ccagaagcag aagtatttgc gttgcctt atgattccta 2276
attttggaaac ctctaaaaaa gcgttgctcg acacaaaatt tggcaaggt ttattgaaa 2336
aaattgataa agagttaaac gtacaagtgt tatctgtggc gtataacggt acacgtcaaa 2396
caacttctaa ccgtcaatc aacagcattt aagacatgaa agggtaaaa ttacgtgtac 2456
ctaacgcggc aaccaacccctt gcttattgcaaa aatacgtggg tgcagcgcacaccaatgg 2516
cattctctga agtttacctt gcgcttcaaa caaactctgt ggatggtcaa gaaaacccat 2576
taccgacaat ccaagcacaa aaattctatg aagtacaaaa atacttagcg ttaactaacc 2636
acatcttaaa tgaccaactt tacttaatca gtaacgatac gttggcagat ttaccagaag 2696
atttacaaaa agtggtaaa gatgcagcag cgaaagccgc tgaatatcact actaaactct 2756
tcgttgcgg tgagaacagc tttagttgaat t 2787

<210> 75
<211> 158
<212> PRT
<213> Pasteurella multocida

<400> 75
Met Val Leu Pro Ile Ile Ser Thr Pro Lys Leu Trp Gln Tyr Ile Pro
1 5 10 15
Ser Ser Lys Leu Glu Gln Ser Ala Met Ala Lys Gln Pro Asn Ser Leu
20 25 30
Ile Arg Leu Ile Met Ala Ser Arg Val Val Gly Arg Thr Arg Ser Val
35 40 45
Pro Ser Lys Ala Ile Ile Ser Ala Pro Ala Ala Asn Ser Ser Met
50 55 60
Ser Cys Lys Asn Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg
65 70 75 80
Leu Thr Ile Pro Ile Ile Gly Thr Leu Thr Thr Leu Arg Val Ala Phe
85 90 95
Lys Phe Ser Ile Pro Ser Ile Arg Asn Pro Ala Ala Pro Pro Ile Thr
100 105 110
Asp Ala Cys Ala Met Ala Ala Thr Ile Ser Gly Glu Ser Ile Gly Pro
115 120 125
Leu Ser Thr Gly Trp Gln Asp Ala Ile Lys Pro Tyr Leu Ile Cys Ser
130 135 140
Lys Thr Cys Gly Cys Asp Ser Phe Asp Ile Leu Thr Pro Val
145 150 155

<210> 76
<211> 2787
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1949)..(2785)

<220>
<223> yiao

<400> 76
gttaacacac catgattaat gatgccgtt gaagccactg caacgtaatc gaattgtccg 60
gcatacaaag caagaatgtt ggccagtgtg tcatgcacatcg cattggcagc atcagcttgt 120
ggcgttgcaa tctgttggcg ttgttctatt ttgccgtctg ttacaatagc cgaggcaatt 180
tttgttccac caatatctaa tgctaaacag cgcataaggct ctccttctgt gatgacttat 240
tttgccgatt tgacggcatc ggcaaaccag cttacgatat gttcgaggcg agtcagcgc 300
gatcctacgg tgacagagta agcacaatc tcaattgcgg ttttcgccaa ttctgggtg 360

ttatagcgcc cttctgccat cactcgccag ccagcagcat tcaaatctt gactaactga 420
taatccggtt cagctggaat ttcaccgcca gtataaccag acatggtgct accaataatt 480
tctaccctta agttgtggca atacatccct tcttcaaaat tagaacaatc cgccatggct 540
aaacaaccta attctttgat tcgtttaata atggcttcac gtgtagttgg acggacgcga 600
tcggtaccat caaaagcaat aatatcgccg cctgctgcgg ctaactcttc aatgtcttgt 660
aaaaatgggc taatacgaac gggactgtca ggtaaatcgc gtttaacgat accaataatc 720
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gcagcaccac cgataacgga tgcttgcgc atggcggcaa caatttctgg cgagtccatt 840
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caacgtaacc aatagaggag aactcata atg aaa ttt aaa aaa cta cta ctt 1972
Met Lys Phe Lys Lys Leu Leu Leu
1 5
gca tct tta tgt tta ggt gtt tca gct tct gta ttt gca gca gat tac 2020
Ala Ser Leu Cys Leu Gly Val Ser Ala Ser Val Phe Ala Ala Asp Tyr
10 15 20
gat ctt aaa ttc ggt atg gtt gcg ggt cca agc tca aac gaa tat aaa 2068
Asp Leu Lys Phe Gly Met Val Ala Gly Pro Ser Ser Asn Glu Tyr Lys
25 30 35 40

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att gat gtg gct att ttc cct agc tca cag tta ggt gat gac cgt gtg Ile Asp Val Ala Ile Phe Pro Ser Ser Gln Leu Gly Asp Asp Arg Val 60 65 70	2164
atg att aaa caa tta aaa gac ggt gca tta gac ttt acg tta ggt gaa Met Ile Lys Gln Leu Lys Asp Gly Ala Leu Asp Phe Thr Leu Gly Glu 75 80 85	2212
tca gca cgt ttc caa att tac ttc cca gaa gca gaa gta ttt gcg ttg Ser Ala Arg Phe Gln Ile Tyr Phe Pro Glu Ala Glu Val Phe Ala Leu 90 95 100	2260
cct tat atg att cct aat ttt gaa acc tct aaa aaa gcg ttg ctc gac Pro Tyr Met Ile Pro Asn Phe Glu Thr Ser Lys Lys Ala Leu Leu Asp 105 110 115 120	2308
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aaa ttc tat gaa gta caa aaa tac tta gcg tta act aac cac atc tta Lys Phe Tyr Glu Val Gln Lys Tyr Leu Ala Leu Thr Asn His Ile Leu 220 225 230	2644
aat gac caa ctt tac tta atc agt aac gat acg ttg gca gat tta cca Asn Asp Gln Leu Tyr Leu Ile Ser Asn Asp Thr Leu Ala Asp Leu Pro 235 240 245	2692
gaa gat tta caa aaa gtg gtt aaa gat gca gca gcg aaa gcc gct gaa Glu Asp Leu Gln Lys Val Val Lys Asp Ala Ala Lys Ala Ala Glu 250 255 260	2740
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<213> Pasteurella multocida

<400> 77

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Gly Pro Ser Ser Asn Glu Tyr Lys Ala Val Glu Phe Phe Ala Lys Glu
35 40 45

Val Lys Glu Lys Ser Asn Gly Lys Ile Asp Val Ala Ile Phe Pro Ser
50 55 60

Ser Gln Leu Gly Asp Asp Arg Val Met Ile Lys Gln Leu Lys Asp Gly
65 70 75 80

Ala Leu Asp Phe Thr Leu Gly Glu Ser Ala Arg Phe Gln Ile Tyr Phe
85 90 95

Pro Glu Ala Glu Val Phe Ala Leu Pro Tyr Met Ile Pro Asn Phe Glu
100 105 110

Thr Ser Lys Lys Ala Leu Leu Asp Thr Lys Phe Gly Gln Gly Leu Leu
115 120 125

Lys Lys Ile Asp Lys Glu Leu Asn Val Gln Val Leu Ser Val Ala Tyr
130 135 140

Asn Gly Thr Arg Gln Thr Thr Ser Asn Arg Ala Ile Asn Ser Ile Glu
145 150 155 160

Asp Met Lys Gly Leu Lys Leu Arg Val Pro Asn Ala Ala Thr Asn Leu
165 170 175

Ala Tyr Ala Lys Tyr Val Gly Ala Ala Pro Thr Pro Met Ala Phe Ser
180 185 190

Glu Val Tyr Leu Ala Leu Gln Thr Asn Ser Val Asp Gly Gln Glu Asn
195 200 205

Pro Leu Pro Thr Ile Gln Ala Gln Lys Phe Tyr Glu Val Gln Lys Tyr
210 215 220

Leu Ala Leu Thr Asn His Ile Leu Asn Asp Gln Leu Tyr Leu Ile Ser
225 230 235 240

Asn Asp Thr Leu Ala Asp Leu Pro Glu Asp Leu Gln Lys Val Val Lys
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Asp Ala Ala Ala Lys Ala Ala Glu Tyr His Thr Lys Leu Phe Val Asp
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Gly Glu Asn Ser Leu Val Glu
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<210> 78

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<212> DNA

<213> Pasteurella multocida

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Met Thr Lys Val Ile His Thr Asp Asn Ala Pro Ala Ala Ile
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ggt cct tat gta caa gcg gta gat tta ggt aat atg ctg tta acc tct 997
Gly Pro Tyr Val Gln Ala Val Asp Leu Gly Asn Met Leu Leu Thr Ser
15 20 25 30

ggg caa att cca gtg aat cca aaa acc ggt gaa gtg cca gcg gat atc 1045
Gly Gln Ile Pro Val Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Ile
35 40 45

gta gca caa gca cgt caa tcg tta gaa aac gtg aaa gcg att gtg gaa 1093
Val Ala Gln Ala Arg Gln Ser Leu Glu Asn Val Lys Ala Ile Val Glu
50 55 60

caa gcg gga tta caa gtc gca aat atc gtg aaa acc acg gtg ttt gtg 1141
Gln Ala Gly Leu Gln Val Ala Asn Ile Val Lys Thr Val Phe Val
65 70 75

aaa gat tta aat gac ttt gca gcg gtc aat gcg gag tat gaa cgt ttc 1189
Lys Asp Leu Asn Asp Phe Ala Ala Val Asn Ala Glu Tyr Glu Arg Phe
80 85 90

ttt aaa gag aac aat cac cct agc ttc cct gct cgt tca tgt gtg gaa 1237

Phe Lys Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu
95 100 105 110

gtg gca cgt ttg ccg aaa gat gtg ggg att gaa atc gag gca atc gct 1285
Val Ala Arg Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala
115 120 125

gta aaa gcc taatgaatag cttgcattta tcttagtcgt agcaaaaacaa 1334
Val Lys Ala

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<212> PRT
<213> Pasteurella multocida

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Tyr Val Gln Ala Val Asp Leu Gly Asn Met Leu Leu Thr Ser Gly Gln

20

25

30

Ile Pro Val Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Ile Val Ala
35 40 45

Gln Ala Arg Gln Ser Leu Glu Asn Val Lys Ala Ile Val Glu Gln Ala
50 55 60

Gly Leu Gln Val Ala Asn Ile Val Lys Thr Thr Val Phe Val Lys Asp
65 70 75 80

Leu Asn Asp Phe Ala Ala Val Asn Ala Glu Tyr Glu Arg Phe Phe Lys
85 90 95

Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu Val Ala
100 105 110

Arg Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala Val Lys
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Ala

<210> 80

<211> 6642

<212> DNA

<213> *Pasteurella multocida*

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<221> CDS

<222> (463)..(1884)

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agttgtttta agagattaac ggaagcaaca ctgatcgacaa aatgcgaag atcgtaaggc 180

gaatttagtt gaaactgtgg gagtgggcg tggataa gctggacttg atgtccttgt 240

ttacgttaagc caagcgcaca ggctgcacca accatgccac cgccaaaccac gatcatgtct 300

ttttgtatga cgtccatagg atttccctt tctttttgtt acgtattcta ccgtcaatga 360

ggaaatttca aaagaaatct ctttttagc tagccagcat aggttcaaga ctgtaaaata 420

gtcagtcaca ttttatagg ttaactgaat ttttaaacg at atg acg caa aaa 474
Met Thr Gln Lys
1

tta cat att aaa acg tgg ggt tgt cag atg aat gaa tat gat tca tct 522
Leu His Ile Lys Thr Trp Gly Cys Gln Met Asn Glu Tyr Asp Ser Ser
5 10 15 20

aaa atg gca gat ctc tta aac agt act cac ggc tta gag tta aca gaa 570
Lys Met Ala Asp Leu Leu Asn Ser Thr His Gly Leu Glu Leu Thr Glu
25 30 35

att ccg gaa gaa gcg gat gtg tta ttc aac act tgc tca att cgt Ile Pro Glu Glu Ala Asp Val Leu Leu Leu Asn Thr Cys Ser Ile Arg	40	45	50	618
gaa aaa gca caa gaa aaa gtt ttc cat caa tta gga cgt tgg aaa gaa Glu Lys Ala Gln Glu Lys Val Phe His Gln Leu Gly Arg Trp Lys Glu	55	60	65	666
tta aag aaa cat aag ccg gga ctc gtt atc ggt gtt ggg ggc tgc gtt Leu Lys His Lys Pro Gly Leu Val Ile Gly Val Gly Gly Cys Val	70	75	80	714
gcc tca caa gaa gga gaa cac att cgt act cgt gct cct tat gtc gat Ala Ser Gln Glu Gly His Ile Arg Thr Arg Ala Pro Tyr Val Asp	85	90	95	762
85	90	95	100	
att att ttt gga cca caa acc tta cat cgt tta cct gaa atg atc aat Ile Ile Phe Gly Pro Gln Thr Leu His Arg Leu Pro Glu Met Ile Asn	105	110	115	810
cag atc aga ggt ggt aaa agc tca gta gtc gat gtc agt ttt cca gaa Gln Ile Arg Gly Gly Lys Ser Ser Val Val Asp Val Ser Phe Pro Glu	120	125	130	858
120	125	130		
att gaa aaa ttc gac cgt tta cca gaa ccg cgt gca gaa ggt cca act Ile Glu Lys Phe Asp Arg Leu Pro Glu Pro Arg Ala Glu Gly Pro Thr	135	140	145	906
135	140	145		
gtc ttc gta tcc att atg gaa ggc tgc ttt aat aaa tat tgc tca ttc tgc Ala Phe Val Ser Ile Met Glu Gly Cys Asn Lys Tyr Cys Ser Phe Cys	150	155	160	954
150	155	160		
gtc gtg cct tat acg cgt ggt gaa gaa gtc agt cgt cca gtg gat gat Val Val Pro Tyr Thr Arg Gly Glu Glu Val Ser Arg Pro Val Asp Asp	165	170	175	1002
165	170	175	180	
gta tta ttt gaa att gca cag ttg gca gag caa ggc gtg cgt gaa gtg Val Leu Phe Glu Ile Ala Gln Leu Ala Glu Gln Gly Val Arg Glu Val	185	190	195	1050
185	190	195		
aat tta tta gga caa aac gtg aac gct tat cgt ggt gca act cat gat Asn Leu Leu Gly Gln Asn Val Asn Ala Tyr Arg Gly Ala Thr His Asp	200	205	210	1098
200	205	210		
gac ggt att tgt act ttt gcg gaa ttg tta cgt tta gta gtc gct att Asp Gly Ile Cys Thr Phe Ala Glu Leu Leu Arg Leu Val Ala Ala Ile	215	220	225	1146
215	220	225		
gat ggt att gac cgt tta cgt ttt acc acc agt cac cca att gag ttc Asp Gly Ile Asp Arg Leu Arg Phe Thr Thr Ser His Pro Ile Glu Phe	230	235	240	1194
230	235	240		
act gat gac att att gat gtg tac cgt gat acg cca gag ttg gtg agt Thr Asp Asp Ile Ile Asp Val Tyr Arg Asp Thr Pro Glu Leu Val Ser	245	250	255	1242
245	250	255	260	
ttc tta cac tta cct gta caa agt ggt tct gat cgt gtg tta tct atg Phe Leu His Leu Pro Val Gln Ser Gly Ser Asp Arg Val Leu Ser Met	265	270	275	1290
265	270	275		
atg aaa cgc aat cat acg gca tta gaa tat aaa tcg att att cgg aag Met Lys Arg Asn His Thr Ala Leu Glu Tyr Lys Ser Ile Ile Arg Lys	280	285	290	1338
280	285	290		

tta aga gcg gtg cgt cca gag att caa att agc tca gat ttt att gtc 1386
Leu Arg Ala Val Arg Pro Glu Ile Gln Ile Ser Ser Asp Phe Ile Val
295 300 305

ggt ttc ccg ggc gaa aca gca gaa gat ttc gag caa acc atg aat tta 1434
Gly Phe Pro Gly Glu Thr Ala Glu Asp Phe Glu Gln Thr Met Asn Leu
310 315 320

att gca caa gta aat ttt gat atg agt ttc agc ttc att tat tca gca 1482
Ile Ala Gln Val Asn Phe Asp Met Ser Phe Ser Phe Ile Tyr Ser Ala
325 330 335 340

cgt cca ggc acg cca gca gca gat atg cct gat gat gtg aca gaa gaa 1530
Arg Pro Gly Thr Pro Ala Ala Asp Met Pro Asp Asp Val Thr Glu Glu
345 350 355

gag aag aaa caa cgt tta tat gtg ttg caa caa cgc att aac aat caa 1578
Glu Lys Lys Gln Arg Leu Tyr Val Leu Gln Gln Arg Ile Asn Asn Gln
360 365 370

gcc gcg caa ttt agt cga gca atg tta ggc aca gaa cag cgc gtg tta 1626
Ala Ala Gln Phe Ser Arg Ala Met Leu Gly Thr Glu Gln Arg Val Leu
375 380 385

gtg gaa gga ccc tcg aaa aaa gat tta atg gaa ctc aca ggg cgt aca 1674
Val Glu Gly Pro Ser Lys Lys Asp Leu Met Glu Leu Thr Gly Arg Thr
390 395 400

gaa act aat cgt atc gtc aat ttt gtg ggc acg cct gat atg att ggg 1722
Glu Thr Asn Arg Ile Val Asn Phe Val Gly Thr Pro Asp Met Ile Gly
405 410 415 420

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Lys Phe Val Asp Ile Lys Ile Thr Asp Val Phe Thr Asn Ser Leu Arg
425 430 435

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Gly Glu Val Val Arg Thr Glu Glu Gln Met Gly Leu Arg Val Val Gln
440 445 450

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Ser Pro Gln Met Val Ile Asn Arg Thr Arg Lys Glu Asp Glu Leu Gly
455 460 465

gtg gga cgt tat cac gcg tagtcgtgct atcccttcaa atatttaacc 1914
Val Gly Arg Tyr His Ala
470

gctctcgagt ttctcaagag cggttatattt ttatgaaaaa ttttgataa attgaccgct 1974

ctttttattt ctccatattt tgatagacag cgtgtttct gttattcattc gtatttctt 2034

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<213> Pasteurella multocida

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35 40 45
Cys Ser Ile Arg Glu Lys Ala Gln Glu Lys Val Phe His Gln Leu Gly
50 55 60
Arg Trp Lys Glu Leu Lys Lys His Lys Pro Gly Leu Val Ile Gly Val
65 70 75 80
Gly Gly Cys Val Ala Ser Gln Glu Gly Glu His Ile Arg Thr Arg Ala
85 90 95
Pro Tyr Val Asp Ile Ile Phe Gly Pro Gln Thr Leu His Arg Leu Pro
100 105 110
Glu Met Ile Asn Gln Ile Arg Gly Gly Lys Ser Ser Val Val Asp Val
115 120 125
Ser Phe Pro Glu Ile Glu Lys Phe Asp Arg Leu Pro Glu Pro Arg Ala
130 135 140
Glu Gly Pro Thr Ala Phe Val Ser Ile Met Glu Gly Cys Asn Lys Tyr
145 150 155 160
Cys Ser Phe Cys Val Val Pro Tyr Thr Arg Gly Glu Glu Val Ser Arg
165 170 175
Pro Val Asp Asp Val Leu Phe Glu Ile Ala Gln Leu Ala Glu Gln Gly
180 185 190
Val Arg Glu Val Asn Leu Leu Gly Gln Asn Val Asn Ala Tyr Arg Gly
195 200 205
Ala Thr His Asp Asp Gly Ile Cys Thr Phe Ala Glu Leu Leu Arg Leu
210 215 220

Val Ala Ala Ile Asp Gly Ile Asp Arg Leu Arg Phe Thr Thr Ser His
225 230 235 240

Pro Ile Glu Phe Thr Asp Asp Ile Ile Asp Val Tyr Arg Asp Thr Pro
245 250 255

Glu Leu Val Ser Phe Leu His Leu Pro Val Gln Ser Gly Ser Asp Arg
260 265 270

Val Leu Ser Met Met Lys Arg Asn His Thr Ala Leu Glu Tyr Lys Ser
275 280 285

Ile Ile Arg Lys Leu Arg Ala Val Arg Pro Glu Ile Gln Ile Ser Ser
290 295 300

Asp Phe Ile Val Gly Phe Pro Gly Glu Thr Ala Glu Asp Phe Glu Gln
305 310 315 320

Thr Met Asn Leu Ile Ala Gln Val Asn Phe Asp Met Ser Phe Ser Phe
325 330 335

Ile Tyr Ser Ala Arg Pro Gly Thr Pro Ala Ala Asp Met Pro Asp Asp
340 345 350

Val Thr Glu Glu Glu Lys Lys Gln Arg Leu Tyr Val Leu Gln Gln Arg
355 360 365

Ile Asn Asn Gln Ala Ala Gln Phe Ser Arg Ala Met Leu Gly Thr Glu
370 375 380

Gln Arg Val Leu Val Glu Gly Pro Ser Lys Lys Asp Leu Met Glu Leu
385 390 395 400

Thr Gly Arg Thr Glu Thr Asn Arg Ile Val Asn Phe Val Gly Thr Pro
405 410 415

Asp Met Ile Gly Lys Phe Val Asp Ile Lys Ile Thr Asp Val Phe Thr
420 425 430

Asn Ser Leu Arg Gly Glu Val Val Arg Thr Glu Glu Gln Met Gly Leu
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<213> Pasteurella multocida

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<222> (407)..(1156)

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Thr Val Val Asn Pro Glu Arg Arg Arg Phe Phe Lys Glu Ala Thr Arg
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act gca ggc ggg ttg gca ggg gtg act ttg ctc ctt ggt ttg caa caa 511
Thr Ala Gly Gly Leu Ala Gly Val Thr Leu Leu Leu Gly Leu Gln Gln
20 25 30 35
aag cag agt ctt gcg cgc gaa ggc gtg gcg tta cgc cca cct ttt gcc 559
Lys Gln Ser Leu Ala Arg Glu Gly Val Ala Leu Arg Pro Pro Phe Ala
40 45 50
ctt gag aat gag aaa gcg ttt tct gct gcg tgc att cgt tgg ggt cag 607
Leu Glu Asn Glu Ala Phe Ser Ala Ala Cys Ile Arg Cys Gly Gln
55 60 65
tgt gta caa gcc tgt cca cat gag atg ttg cat ctt gcc tca ctg att 655
Cys Val Gln Ala Cys Pro His Glu Met Leu His Leu Ala Ser Leu Ile
70 75 80
tca ccg atg gaa gca ggt aca ccg tat ttc att gcg cgc gat aag ccc 703
Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg Asp Lys Pro
85 90 95
tgt gaa atg tgt gtg gat att cct tgt gca aaa gcc tgc cca acc ggt 751
Cys Glu Met Cys Val Asp Ile Pro Cys Ala Lys Ala Cys Pro Thr Gly
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120 125 130
gct gtc ctg cta gat cat gaa act tgt ctg aac tgg caa ggt tta cgc 847
Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln Gly Leu Arg
135 140 145
tgt gat gtg tgt tat cgc gtc tgt ccg ctg att aat aaa gcg att acg 895
Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asn Lys Ala Ile Thr
150 155 160
tta gtg atg cat cgt aat gag cgt acg ggt aag cac gcc gtc ttt atc 943
Leu Val Met His Arg Asn Glu Arg Thr Gly Lys His Ala Val Phe Ile
165 170 175
cca aca gtg cat tcc gaa gcc tgt aca gga tgt ggc aaa tgt gaa gaa 991
Pro Thr Val His Ser Glu Ala Cys Thr Gly Cys Gly Lys Cys Glu Glu
180 185 190 195
gct tgc gtt cta gaa gaa gcg gca atc aaa gtg tta ccg atg gca tta 1039

Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro Met Ala Leu
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gcg aaa ggc atg tta ggt aaa cat tac cgt tta ggt tgg gaa gag aaa 1087
Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp Glu Glu Lys
215 220 225

gaa aaa gcc ggg cat tcc ctt gcg cca gaa ggc att att tct ctc ccg 1135
Glu Lys Ala Gly His Ser Leu Ala Pro Glu Gly Ile Ile Ser Leu Pro
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Thr Arg Leu Pro Glu Ser Leu
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<212> PRT
<213> Pasteurella multocida

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35 40 45
Pro Phe Ala Leu Glu Asn Glu Lys Ala Phe Ser Ala Ala Cys Ile Arg
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Cys Gly Gln Cys Val Gln Ala Cys Pro His Glu Met Leu His Leu Ala
65 70 75 80
Ser Leu Ile Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg
85 90 95
Asp Lys Pro Cys Glu Met Cys Val Asp Ile Pro Cys Ala Lys Ala Cys
100 105 110
Pro Thr Gly Ala Leu Asp Asn Gln Ala Thr Glu Ile Asp Asp Ala Arg
115 120 125
Met Gly Leu Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln
130 135 140
Gly Leu Arg Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asn Lys
145 150 155 160
Ala Ile Thr Leu Val Met His Arg Asn Glu Arg Thr Gly Lys His Ala
165 170 175
Val Phe Ile Pro Thr Val His Ser Glu Ala Cys Thr Gly Cys Gly Lys
180 185 190
Cys Glu Glu Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro
195 200 205
Met Ala Leu Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp
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Ser Leu Pro Thr Arg Leu Pro Glu Ser Leu

245

250

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Met Thr Lys Leu Ser Ile Gln Arg Asp Asn Leu Ile Cys
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Glu Leu Thr Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro
65 70 75
agt tca agt tta ggt ttc tta ata ttg aaa act gta cca tct ttt tca 2689
Ser Ser Ser Leu Gly Phe Leu Ile Leu Lys Thr Val Pro Ser Phe Ser
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Tyr Val Thr Ile Ser Thr Leu Asn Arg Val
95 100
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gactgcaagc gacttggttt cattgctaac cgtctgctca agtgcgtgtga ttttggatgt 3159
taaatctaac ttagttgcat tgacttcatc agtccattct gactttaact ctttctcgc 3219
aagtgacgccc acttcatctt tgctagctt cgtttctttt aagtcagaaa tgccactagt 3279
attttgcgcc actttagaat cgagcgtttc tagtttgta gagaaagatt tgtcttttc 3339
gctagccgtt ttttgaatta gctgtatttc actttcgctc aatccaactc tagcagttag 3399
actgtctagc ttgtcagcag tagatttatt cacagtcgct tgtgattgct tgtgttgaat 3459
aatatcccgcg cttacttccg agatagccac gtcga 3494

<210> 85

<211> 103

<212> PRT

<213> *Pasteurella multocida*

<400> 85

Met Thr Lys Leu Ser Ile Gln Arg Asp Asn Leu Ile Cys Leu Ser Tyr
1 5 10 15

Val Ala Leu Met Gly Phe Gly Phe Pro Ile Met Arg Tyr Met Ser Ile
20 25 30

His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu Ser Gly Gly
35 40 45

Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala Glu Leu Thr
50 55 60

Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro Ser Ser Ser
65 70 75 80

Leu Gly Phe Leu Ile Leu Lys Thr Val Pro Ser Phe Ser Tyr Val Thr
85 90 95

Ile Ser Thr Leu Asn Arg Val
100

<210> 86

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PRIMER

<400> 86

aggccggtac cggccgcct

<210> 87
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 87
cggccggtagc cggccctagg 19

<210> 88
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 88
catggtagcc attctaac 18

<210> 89
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 89
ctaggtacctt acaacacctc 18

<210> 90
<211> 119
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: transposon
insert

<220>
<223> Nucleotides designated "n" are A, T, G or C.

<400> 90
ctaggtacctt acaacacctt gcttnknknk nknknknknk nknknknknk nknknknknk 60
nknknknknk nknknknknk nknknknknk nknkaagctt ggtagaaatg ggtaccatg 119

<210> 91
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 91

tacctacaac ctcaagct	18
<210> 92	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: primer	
<400> 92	
tacccattct aaccaagc	18
<210> 93	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: primer	
<400> 93	
tacctacaac ctcaagctt	19
<210> 94	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: primer	
<400> 94	
tacccattct aaccaagctt	20
<210> 95	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: primer	
<400> 95	
ggcagagcat tacgctgac	19
<210> 96	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: primer	
<400> 96	
gtaccggcca ggcggccacg cgtattc	27

<210> 97
<211> 531
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> *atpG*

<400> 97
tggtagttt ggttttagtag ggtcgaaagg cgtaagcttt tacaaaatc taggcttaaa 60
cgttagatct caagtaacgg gattaggcga taatccggaa atggaacgta tcgtgggcgc 120
agttaatgaa atgattaatg cgttccgaaa cggagaagtg gatgcggttt acgtcgctta 180
caaccgtttt gaaaatacga tgtcacaaaa acctgttac gcacagttac ttccgttacc 240
taaactagat gacgatgaat tagatacga aagttcatgg gattatattt atgaaccgaa 300
tccacaagtt ttattggata gtttacttgt tcgttattta gaaactcagg tataccaagc 360
agttgtagat aacctagctt ctgaacaagc cgctcgaatg gtagcgatga aagccgcaac 420
agataatgcg ggtacattaa tcgatgaatt acaatttagtg tataacaaag ctcgccaagc 480
aaggcattaca aatgaattaa acgaaattgt tgccggtgcc gcagcaattt a 531

<210> 98
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 98
tctccattcc cttgctgcgg caccc 25

<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 99
ggattacagc cggatccggg 20

<210> 100
<211> 1034
<212> DNA
<213> *Pasteurella multocida*

<220>
<223> *cap5E*

<220>
<221> CDS
<222> (1)..(1032)

<400> 100
atg ttt aaa aat aaa aca ctt tta att aca ggt gga acg ggt tct ttt 48
Met Phe Lys Asn Lys Thr Leu Leu Ile Thr Gly Gly Thr Gly Ser Phe
1 5 10 15

ggt aat gct gta ctc aaa cgt ttc tta gaa aca gat att cga gaa att 96
Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile
20 25 30

cgt gtt ttt tcg cgt gat gag aag aaa caa gat gac atg cggt aaa aaa 144
Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys
35 40 45

tat aat gat gca aaa tta aaa ttt tat att ggc gat gtt cgt gac tac 192
Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr
50 55 60

gat agt att tta aat gcc tcg cga ggt gtt gac tat att tat cat gct 240
Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala
65 70 75 80

gcc gca tta aag caa gtg cct tca tgc gag ttt tat ccg tta gag gca 288
Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala
85 90 95

gtg aaa acc aat att tta ggt acg gca aat gtc tta gaa gcc gcc atc 336
Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ala Ile
100 105 110

caa aac cag ata aaa cgc gtc gtc tgt ctt agc aca gat aaa gcg gtg 384
Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val
115 120 125

tac cca att aat gcg atg ggc att tct aaa gca atg atg gaa aaa gtc 432
Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val
130 135 140

atc atc gca aaa tcg cgt aac cta gaa ggc aca cca acg aca atc tgt 480
Ile Ile Ala Lys Ser Arg Asn Leu Glu Gly Thr Pro Thr Thr Ile Cys
145 150 155 160

tgt act cgc tat ggc aat gtc atg gca tcg cgt ggt tcg gtt atc cca 528
Cys Thr Arg Tyr Gly Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro
165 170 175

tta ttt gtc gat caa ata cgt caa ggc aag cct ttt act att act gat 576
Leu Phe Val Asp Gln Ile Arg Gln Gly Lys Pro Phe Thr Ile Thr Asp
180 185 190

cct gag atg aca cgc ttt atg atg aca ttg gaa gat gct gtg gat tta 624
Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu
195 200 205

gtc cta tat gca ttt aaa aat ggt caa aat ggt gat gtt ttt gta caa 672
Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln
210 215 220

aaa gcc ccc gca gca acc att ggt acc ctt gcc aaa gca att acc gaa 720
Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu
225 230 235 240

tta tta tct gtc cca aat cac cct att tcc att ata ggt acg cgt cat 768
Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His

	245	250	255	
gga gag aaa gca ttc gaa gct tta tta agc cgt gaa gaa atg gtt cat				816
Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His				
260	265	270		
gca att aat gaa ggt aat tat tat cgc atc cca gcc gat caa cgc agt				864
Ala Ile Asn Glu Gly Asn Tyr Tyr Arg Ile Pro Ala Asp Gln Arg Ser				
275	280	285		
tta aat tac agt aaa tat gtc gaa aaa ggg gaa cca aaa att acc gaa				912
Leu Asn Tyr Ser Lys Tyr Val Glu Lys Gly Glu Pro Lys Ile Thr Glu				
290	295	300		
gtc acc gac tac aac tca cat aat act gag cgt ttg act gtc aag gaa				960
Val Thr Asp Tyr Asn Ser His Asn Thr Glu Arg Leu Thr Val Lys Glu				
305	310	315	320	
atg aag cag tta ctg ctt aaa ctt gaa ttc ata cag aaa atg att gag				1008
Met Lys Gln Leu Leu Lys Leu Glu Phe Ile Gln Lys Met Ile Glu				
325	330	335		
ggt gaa tac atc tca ccg gag gta ta				1034
Gly Glu Tyr Ile Ser Pro Glu Val				
340				

<210> 101
<211> 344
<212> PRT
<213> Pasteurella multocida

<400> 101				
Met Phe Lys Asn Lys Thr Leu Leu Ile Thr Gly Gly Thr Gly Ser Phe				
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Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile				
20	25	30		
Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys				
35	40	45		
Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr				
50	55	60		
Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala				
65	70	75	80	
Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala				
85	90	95		
Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ala Ile				
100	105	110		
Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val				
115	120	125		
Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val				
130	135	140		
Ile Ile Ala Lys Ser Arg Asn Leu Glu Gly Thr Pro Thr Thr Ile Cys				
145	150	155	160	

Cys Thr Arg Tyr Gly Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro
165 170 175

Leu Phe Val Asp Gln Ile Arg Gln Gly Lys Pro Phe Thr Ile Thr Asp
180 185 190

Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu
195 200 205

Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln
210 215 220

Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu
225 230 235 240

Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His
245 250 255

Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His
260 265 270

Ala Ile Asn Glu Gly Asn Tyr Tyr Arg Ile Pro Ala Asp Gln Arg Ser
275 280 285

Leu Asn Tyr Ser Lys Tyr Val Glu Lys Gly Glu Pro Lys Ile Thr Glu
290 295 300

Val Thr Asp Tyr Asn Ser His Asn Thr Glu Arg Leu Thr Val Lys Glu
305 310 315 320

Met Lys Gln Leu Leu Lys Leu Glu Phe Ile Gln Lys Met Ile Glu
325 330 335

Gly Glu Tyr Ile Ser Pro Glu Val
340

<210> 102

<211> 4931

<212> DNA

<213> Pasteurella multocida

<220>

<223> fhaB2

<220>

<221> CDS

<222> (1)..(4929)

<220>

<223> Nucleotide at position 4894 is A, T, G, or C. The
corresponding amino acid is unknown.

<400> 102

atg aac aaa aat cgt tac aaa ctc att ttt agt caa gtc aaa ggt tgt 48
Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Gln Val Lys Gly Cys
1 5 10 15

ctc gtt cct gtg gca gaa tgt att aac tca gct att agc aat ggt tca 96
Leu Val Pro Val Ala Glu Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser
20 25 30

tct gat tca aca tcc aca tca gaa caa gtt gaa gag gaa cct ttc ctt 144

Ser	Asp	Ser	Thr	Ser	Thr	Ser	Glu	Gln	Val	Glu	Glu	Glu	Pro	Phe	Leu		
35						40						45					
cta	gaa	caa	tat	tca	ctt	tcc	gtc	tct	tta	tta	gta	aaa	agc	acg		192	
Leu	Glu	Gln	Tyr	Ser	Leu	Ser	Ser	Val	Ser	Leu	Leu	Val	Lys	Ser	Thr		
50					55					60							
ttc	aat	cct	gtt	tgc	tat	gca	atg	caa	ttg	act	tgg	aaa	cag	ctt	tct		240
Phe	Asn	Pro	Val	Ser	Tyr	Ala	Met	Gln	Leu	Thr	Trp	Lys	Gln	Leu	Ser		
65					70					75			80				
att	tta	ttt	tta	act	gtg	att	tct	gtt	cct	gtt	ttg	gct	gag	gga	aaa		288
Ile	Leu	Phe	Leu	Thr	Val	Ile	Ser	Val	Pro	Val	Leu	Ala	Glu	Gly	Lys		
85					90					95							
ggg	gat	gaa	aga	aat	caa	tta	aca	gtg	att	gat	aat	agc	gat	cat	att		336
Gly	Asp	Glu	Arg	Asn	Gln	Leu	Thr	Val	Ile	Asp	Asn	Ser	Asp	His	Ile		
100			.		105					110							
aaa	tta	gat	gca	tct	aat	ctt	gct	ggt	aat	gat	aaa	aca	aaa	atc	tat		384
Lys	Leu	Asp	Ala	Ser	Asn	Leu	Ala	Gly	Asn	Asp	Lys	Thr	Lys	Ile	Tyr		
115					120					125							
caa	gca	gaa	aat	aaa	gtt	ctg	gtt	att	gat	att	gct	aaa	cca	aat	ggg		432
Gln	Ala	Glu	Asn	Lys	Val	Leu	Val	Ile	Asp	Ile	Ala	Lys	Pro	Asn	Gly		
130					135					140							
aaa	ggg	att	tca	gat	aac	cgt	ttt	gaa	aaa	ttt	aat	att	cca	aat	agc		480
Lys	Gly	Ile	Ser	Asp	Asn	Arg	Phe	Glu	Lys	Phe	Asn	Ile	Pro	Asn	Ser		
145					150					155			160				
gcg	gtg	ttt	aat	aat	aat	ggg	act	gaa	gct	cag	gca	aga	tca	aca	tta		528
Ala	Val	Phe	Asn	Asn	Gly	Thr	Glu	Ala	Gln	Ala	Arg	Ser	Thr	Leu			
165					170					175							
att	ggt	tac	att	ccg	caa	aat	caa	aat	tta	agg	gga	ggg	aaa	gaa	gct		576
Ile	Gly	Tyr	Ile	Pro	Gln	Asn	Gln	Asn	Leu	Arg	Gly	Gly	Lys	Glu	Ala		
180					185					190							
gat	gtt	ata	tta	aat	caa	gtg	aca	ggt	cct	caa	gaa	agt	aaa	att	gtt		624
Asp	Val	Ile	Leu	Asn	Gln	Val	Thr	Gly	Pro	Gln	Glu	Ser	Lys	Ile	Val		
195					200					205							
ggc	gct	ttt	gaa	gta	tta	ggt	aaa	aaa	gct	gat	atc	gtc	att	gca	aac		672
Gly	Ala	Leu	Glu	Val	Leu	Gly	Lys	Lys	Ala	Asp	Ile	Val	Ile	Ala	Asn		
210					215					220							
caa	aat	ggt	att	acc	tta	aat	ggt	gta	aga	aca	ata	aat	tca	gat	cgt		720
Gln	Asn	Gly	Ile	Thr	Leu	Asn	Gly	Val	Arg	Thr	Ile	Asn	Ser	Asp	Arg		
225					230					235			240				
ttt	gtt	gcc	act	acg	agt	gag	ctt	ata	gat	ccg	aat	cag	atg	atg	tta		768
Phe	Val	Ala	Thr	Ser	Glu	Leu	Ile	Asp	Pro	Asn	Gln	Met	Met	Leu			
245					250					255			255				
aag	gtt	aca	aaa	gga	aat	gtg	atc	att	gat	att	gat	ggt	ttt	tcg	aca		816
Lys	Val	Thr	Lys	Gly	Asn	Val	Ile	Ile	Asp	Ile	Asp	Gly	Phe	Ser	Thr		
260					265					270							
gat	gga	tta	aag	tat	tta	gat	att	att	gct	aaa	aaa	att	gaa	caa	aag		864
Asp	Gly	Leu	Lys	Tyr	Leu	Asp	Ile	Ile	Ala	Lys	Lys	Ile	Glu	Gln	Lys		
275					280					285							

caa tca att aca tca ggg gat aat tca gaa gca aaa aca gat gtc act	912
Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr	
290 295 300	
ctt att gcg ggt tcc agt gaa tat gat tta agc aaa cat gag ctg aaa	960
Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys	
305 310 315 320	
aaa acg agc ggt gaa aat gta tct aat gat gtt att gct atc acg gga	1008
Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly	
325 330 335	
tct agt aca ggc gca atg cat ggt aaa aat att aag ttg att gtg aca	1056
Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr	
340 345 350	
gat aaa ggt gca ggc gta aaa cat gat gga att att ttg tct gaa aat	1104
Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn	
355 360 365	
gat att cag att gaa atg aat gaa ggt gac tta gaa ctt ggc aat acg	1152
Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr	
370 375 380	
att cag caa aca gtg gta aaa aaa gac cga aat att cga gcc aag aaa	1200
Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys	
385 390 395 400	
aaa att gaa gtg aaa aac gct aat cgt gtt ttt gtt ggt agt caa acg	1248
Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr	
405 410 415	
aaa tca gat gaa att tcg tta gag gcg aaa caa gtt aaa atc aga aaa	1296
Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys	
420 425 430	
aac gca gag att agg agt acg aca caa gcc aaa atc gta gca aag ggt	1344
Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly	
435 440 445	
gcc ctg tct att gag caa aat gcg aag ctc gtc gct aaa aag ata gat	1392
Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp	
450 455 460	
gtg gca aca gaa act cta act aat gct ggg cgt att tat ggt cga gag	1440
Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu	
465 470 475 480	
gtt aag ctt gac act aat aat ttg att aat gat aaa gaa att tat gct	1488
Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala	
485 490 495	
gaa cgg aaa ttg agt att ttg acg aaa gga aaa gat ctt gaa att att	1536
Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile	
500 505 510	
caa gat aga tat ttg tct cca ctg atg cgc gta aaa agt agt gtc cgc	1584
Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg	
515 520 525	
ttt tta ggc tct ccg ttt ttc tca ata tct ccg tcg atg ctc gca agc	1632
Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser	
530 535 540	

ctt	agt	gca	cag	ttt	aag	cct	ggg	ttt	gtg	aat	aag	gga	ctc	att	gaa	1680
Leu	Ser	Ala	Gln	Phe	Lys	Pro	Gly	Phe	Val	Asn	Lys	Gly	Leu	Ile	Glu	
545				550				555						560		
agt	gcg	ggg	agt	gca	gaa	tta	act	ttt	aaa	gaa	aaa	acc	agt	ttt	tta	1728
Ser	Ala	Gly	Ser	Ala	Glu	Leu	Thr	Phe	Lys	Glu	Lys	Thr	Ser	Phe	Leu	
				565				570						575		
aca	gag	ggc	aat	aat	ttt	att	aga	gct	aaa	gat	gcg	tta	act	att	aac	1776
Thr	Glu	Gly	Asn	Asn	Phe	Ile	Arg	Ala	Lys	Asp	Ala	Leu	Thr	Ile	Asn	
				580				585						590		
gcc	caa	aat	att	gaa	att	gat	aaa	aat	caa	gat	att	caa	ttg	ggt	gct	1824
Ala	Gln	Asn	Ile	Glu	Ile	Asp	Lys	Asn	Gln	Asp	Ile	Gln	Leu	Gly	Ala	
				595				600						605		
aat	ata	acg	ttg	aat	gtg	gaa	gaa	aac	ttt	gtt	aat	cgt	gca	gga	aca	1872
Asn	Ile	Thr	Leu	Asn	Val	Glu	Glu	Asn	Phe	Val	Asn	Arg	Ala	Gly	Thr	
				610				615						620		
ctg	gca	act	ggt	aaa	aca	ctg	aca	att	aat	acc	gaa	agt	ggc	agt	att	1920
Leu	Ala	Thr	Gly	Lys	Thr	Leu	Thr	Ile	Asn	Thr	Glu	Ser	Gly	Ser	Ile	
				625				630						640		
tac	aat	ctt	ggt	ggg	aca	tta	ggt	gct	gga	aaa	tca	tta	aaa	ctg	act	1968
Tyr	Asn	Leu	Gly	Gly	Thr	Leu	Gly	Ala	Gly	Lys	Ser	Leu	Lys	Leu	Thr	
				645				650						655		
gct	aaa	tca	acg	gaa	gaa	ggt	atg	gga	aat	att	gtt	aac	caa	gaa	aac	2016
Ala	Lys	Ser	Thr	Glu	Glu	Gly	Met	Gly	Asn	Ile	Val	Asn	Gln	Glu	Asn	
				660				665						670		
ggt	tta	ttc	cat	aca	ctc	ggt	aat	atg	atg	tta	gaa	gca	gag	cgt	tct	2064
Gly	Leu	Phe	His	Thr	Leu	Gly	Asn	Met	Met	Leu	Glu	Ala	Glu	Arg	Ser	
				675				680						685		
gtt	tat	aat	att	ggc	gat	att	tat	gct	agt	aaa	aaa	tta	aca	gtt	cat	2112
Val	Tyr	Asn	Ile	Gly	Asp	Ile	Tyr	Ala	Ser	Lys	Lys	Leu	Thr	Val	His	
				690				695						700		
act	cat	aat	ttg	att	aat	gat	gtg	cgt	tta	tct	ggc	aat	gtg	agt	tat	2160
Thr	His	Asn	Leu	Ile	Asn	Asp	Val	Arg	Leu	Ser	Gly	Asn	Val	Ser	Tyr	
				705				710						720		
aag	cct	atc	ggt	tca	agt	cgt	gat	tat	gat	atc	agt	cgt	gtt	gcg	gta	2208
Lys	Pro	Ile	Gly	Ser	Ser	Arg	Asp	Tyr	Asp	Ile	Ser	Arg	Val	Ala	Val	
				725				730						735		
cat	ggt	tgg	cac	aat	aat	gtt	tat	aag	ctc	aac	tta	aat	ctg	caa	gaa	2256
His	Gly	Trp	His	Asn	Asn	Val	Tyr	Lys	Leu	Asn	Leu	Asn	Leu	Gln	Glu	
				740				745						750		
caa	gat	aaa	acc	gat	att	aaa	gtt	gtg	aaa	atg	ggg	gct	atc	cgt	tct	2304
Gln	Asp	Lys	Thr	Asp	Ile	Lys	Val	Val	Lys	Met	Gly	Ala	Ile	Arg	Ser	
				755				760						765		
gat	ggt	gat	ttt	gac	ttt	aag	gga	ata	aag	gcg	aca	tca	tca	gaa	tca	2352
Asp	Gly	Asp	Phe	Asp	Phe	Lys	Gly	Ile	Lys	Ala	Thr	Ser	Ser	Glu	Ser	
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aaa	ccg	cag	tta	att	aat	cat	gga	tta	att	aat	gtc	aaa	gga	aca	ttt	2400
Lys	Pro	Gln	Leu	Ile	Asn	His	Gly	Leu	Ile	Asn	Val	Lys	Gly	Thr	Phe	
				785				790						800		

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Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln	
805 810 815	
aat gca tta gca agc gtg ttt aag aat cca gcg aaa atc acg atg tac	2496
Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr	
820 825 830	
tat caa cca ctt act cgt tat att tgg aca cca tta tcg ggt aat gca	2544
Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala	
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tcg cgt gaa ttt aac aat tta gag tct ttc ctc gat gcc ttg ttt ggc	2592
Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly	
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tca aca aca atc tta aaa tca agt ttc tat agt acg gaa aat ttt agt	2640
Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser	
865 870 875 880	
gct tat cag ctt cta tct cat att cag cat tca cca atg tac caa aaa	2688
Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys	
885 890 895	
gcg atg gca caa gtg ttt ggt gca gag tgg cat agt aaa tcc tat gat	2736
Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp	
900 905 910	
gag atg cga aac aaa tgg aaa agc ttt aaa gaa aat cca aca gat ttc	2784
Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe	
915 920 925	
att tat tac cca tca gaa aaa gca aaa atc cta gcg gga aaa cta gaa	2832
Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu	
930 935 940	
ggt aag ctt aca acg cta caa aat ggt gaa tat gcc gaa cgt ggt aag	2880
Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys	
945 950 955 960	
ttt gat gag agt atc caa att ggt aaa cac caa tta tcg cta cca tca	2928
Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser	
965 970 975	
gta gag ctt aaa gcg gag ttt agt gat aaa gaa cgt ttg gaa gag gac	2976
Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp	
980 985 990	
ggg gta gat tta tcc tcg atc gcc gaa ctc tta gaa atg cca aac tta	3024
Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu	
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Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Leu Ser Pro Ile	
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gag gat cta gat gaa gaa cca cgt aaa aat ctg gat ata gaa gaa agc	3120
Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser	
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ccc gat gat aag ctg ggt ata agt cgt gat gat cgt gga aat aaa cca Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro 1075 1080 1085	3264
cct cgt act gat cct aca gtt gat tat ctt aac cct gat gaa ttc ttt Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe 1090 1095 1100	3312
gaa aat ggt tat ctc ttg aat gag cta cta cag gag ctt gga gaa gag Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu 1105 1110 1115 1120	3360
ccg tta cta aaa gaa ggg gaa gat cat ttt aaa cgt tct acc aat cta Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu 1125 1130 1135	3408
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gag ggg tat ttt gat ctg cct ggt aca tta gat atg aaa ctg cag gag Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu 1155 1160 1165	3504
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act gat cca ctt ttc cgt aca aaa ttg aaa tat atc aat caa gat gac Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp	3984
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ggt cat caa aaa gta aat gtg tta ggg gat aac tat ttt gat cat caa Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln	4080
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1365 1370 1375	
aaa tac aat ctc agc gat gtg gaa tta gtt aaa cag ctg atg gac aat Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn	4176
1380 1385 1390	
tcc aca aca caa gcg cag gag ttg gat ttg aaa cta ggt gcg gca tta Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu	4224
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1445 1450 1455	
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1460 1465 1470	
aat acc ggg aca tta gct ggg aga aaa ctc aat gtt gaa gca gtc aat Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn	4464
1475 1480 1485	
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1490 1495 1500	
gtc ggg cgt aaa ggt att gaa aac gta tct cgt tca ttt gca aat gat Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp	4560
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gaa tta gga gtc act gca caa cgc tca gaa atc aaa acg gaa ggt cat Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His	4608
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Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro	
1570 1575 1580	
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Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro	
1585 1590 1595 1600	
ctt tta ggc gtg tcc gtc tcc atc cag ttt att cag agc ata cta gtg	4848
Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val	
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Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa	
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Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu	
35 40 45	

Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr	
50 55 60	

Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser	
65 70 75 80	

Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys	
85 90 95	

Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile	
100 105 110	

Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr	
115 120 125	

Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly	
130 135 140	

Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser	
145 150 155 160	

Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu	
165 170 175	

Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala	
180 185 190	

Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val
195 200 205

Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn
210 215 220

Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg
225 230 235 240

Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu
245 250 255

Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr
260 265 270

Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys
275 280 285

Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr
290 295 300

Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys
305 310 315 320

Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly
325 330 335

Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr
340 345 350

Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn
355 360 365

Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr
370 375 380

Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys
385 390 395 400

Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr
405 410 415

Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys
420 425 430

Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly
435 440 445

Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp
450 455 460

Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu
465 470 475 480

Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala
485 490 495

Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile
500 505 510

Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg
515 520 525

Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser
530 535 540

Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu
545 550 555 560

Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu
565 570 575

Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn
580 585 590

Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala
595 600 605

Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr
610 615 620

Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile
625 630 635 640

Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr
645 650 655

Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn
660 665 670

Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser
675 680 685

Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His
690 695 700

Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr
705 710 715 720

Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val
725 730 735

His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu
740 745 750

Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser
755 760 765

Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser
770 775 780

Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe
785 790 795 800

Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln
805 810 815

Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr
820 825 830

Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala
835 840 845

Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly
850 855 860

Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser
865 870 875 880

Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys
885 890 895

Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp
900 905 910

Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe
915 920 925

Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu
930 935 940

Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys
945 950 955 960

Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser
965 970 975

Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Asp
980 985 990

Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu
995 1000 1005

Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Leu Ser Pro Ile
1010 1015 1020

Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser
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His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser
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Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met
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Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro
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Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe
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Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu
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Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu
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Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys
1140 1145 1150

Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu
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Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg
1170 1175 1180

Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys Arg Val
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Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu Lys Lys
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Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala Glu Gln
1250 1255 1260

Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp Ile Glu
1265 1270 1275 1280

Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser
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Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu
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Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp
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Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys
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Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln
1345 1350 1355 1360

Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln
1365 1370 1375

Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn
1380 1385 1390

Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu
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Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val
1410 1415 1420

Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe
1425 1430 1435 1440

Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr
1445 1450 1455

Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val
1460 1465 1470

Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn
1475 1480 1485

Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu
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Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp
1505 1510 1515 1520

Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His
1525 1530 1535

Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser
1540 1545 1550

Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu
1555 1560 1565

Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro
1570 1575 1580

Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro
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Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val
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<211> 2009

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<400> 104

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Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
35 40 45

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Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
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Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser
85 90 95

aaa aac aga gaa tat cgt caa gtc atc gga gtt gga ggg aaa ggg gaa 336
Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu
100 105 110

cac ttt ttt ggt ttt gta caa tta acc aaa cgt tgg ggg cat gaa aca	384
His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr	
115 120 125	
atc aac aac ggc aaa ggt aca gac att ctc ggc gaa cat cga ggt aaa	432
Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys	
130 135 140	
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Pro Asn Pro Leu Asn Tyr Tyr Thr Ser Trp Leu Thr Lys Val Gly	
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Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg	
165 170 175	
cgt gaa aag aag ctt acc gaa gaa aaa aca tta ggg ctt agt gat gca	576
Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala	
180 185 190	
gtg cgt ttt gct aat gat caa acc cct tat ctc cgt tat ggt att gaa	624
Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu	
195 200 205	
tat cga tat aac ggc ttg tct tgg ttg gaa acg gta aag ctt ttt ttg	672
Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu	
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Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile	
225 230 235 240	
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Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser Phe Val Tyr Leu Gln	
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Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr Ser Pro Leu Tyr Trp	
260 265 270	
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Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys	
275 280 285	
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Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile	
290 295 300	
aat aga ttc aga caa caa ggt cga aat aac tat aca gaa gtg ttt ccc	960
Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro	
305 310 315 320	
gtt aaa tcc cga gag ttt tct ttt tct ctt atg gac gac att aag att	1008
Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile	
325 330 335	
ggc gaa ttg cta cat ctc gga ttg ggc ggt cgg tgg gat cac tat aac	1056
Gly Glu Leu Leu His Leu Gly Leu Gly Arg Trp Asp His Tyr Asn	
340 345 350	
tat aag cca tta tta aat tct cag cat aat atc aac agg aca cag aga	1104
Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg	
355 360 365	

tta cct tat cca aaa aca tca tcc aaa ttt tcg tat caa ttg agt tta	1152
Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser Tyr Gln Leu Ser Leu	
370 375 380	
gag tat caa tta cat cca tca cat caa att gca tac cgt tta agt acc	1200
Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr	
385 390 395 400	
ggt ttt agg gtt ccc cgt gtt gaa gat ctt tat ttt gaa gac cga gga	1248
Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly	
405 410 415	
aaa agt tct tca caa ttt ctt cct aac ccc gat cta caa ccg gaa act	1296
Lys Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr	
420 425 430	
gca ctg aat cat gaa ata agt tac cgt ttc caa aat caa tat gcc cat	1344
Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His	
435 440 445	
ttc agc gtc ggg ctt ttc cgt aca cgt tat cat aac ttt att caa gaa	1392
Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu	
450 455 460	
cgt gag atg acc tgt gat aaa att cca tat gag tat aat agg act tat	1440
Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr	
465 470 475 480	
gga tat tgc acg cat aat act tat gta atg ttt gtt aat gaa cct gaa	1488
Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu	
485 490 495	
gcc gtg att aaa ggg gtt gaa gta agc ggt gct tta aat ggg tcg gca	1536
Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala	
500 505 510	
ttc gga ctt tcc gac ggt tta act ttc cgt ctc aaa ggg agc tac agc	1584
Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser	
515 520 525	
aaa ggt caa aat cat gac ggc gat ccg tta aaa tct att caa cca tgg	1632
Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp	
530 535 540	
aca gtg gta acc ggt att gat tac gaa act gaa ggg tgg agc gtg agt	1680
Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser	
545 550 555 560	
ttg agc ggg cgt tat agt gcg gct aaa aaa gcc aaa gat gcg ata gaa	1728
Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu	
565 570 575	
acg gaa tac aca cat gat aaa aag gtt gtc aaa caa tgg ccg cat tta	1776
Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu	
580 585 590	
agt cca tcc tac ttt gtt gat ttt acg ggg caa gtt aac ctc agt	1824
Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser	
595 600 605	
aaa aat gtc att ttg aat atg ggg gta ttt aac ttg ttc aat cgt gat	1872
Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp	
610 615 620	

tat atg acg tgg gac agt gca tat aac ttg ttt act agg ggg tat act 1920
Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr
625 630 635 640

tcc cgt tct gtc cgt gct aac agc cca ggc att aat cgg ttt acc gca 1968
Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala
645 650 655

cca aaa cgt aat ttt gct gcc tcg gtg gaa att cgt ttt ta 2009
Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe
660 665

<210> 105
<211> 669
<212> PRT
<213> Pasteurella multocida

<400> 105
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Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu
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Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
35 40 45

Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala
50 55 60

Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
65 70 75 80

Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser
85 90 95

Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu
100 105 110

His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr
115 120 125

Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys
130 135 140

Pro Asn Pro Leu Asn Tyr Tyr Thr Ser Trp Leu Thr Lys Val Gly
145 150 155 160

Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg
165 170 175

Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala
180 185 190

Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu
195 200 205

Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu
210 215 220

Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile
225 230 235 240

Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser Phe Val Tyr Leu Gln
245 250 255

Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr Ser Pro Leu Tyr Trp
260 265 270

Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys
275 280 285

Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile
290 295 300

Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro
305 310 315 320

Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile
325 330 335

Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg Trp Asp His Tyr Asn
340 345 350

Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg
355 360 365

Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser Tyr Gln Leu Ser Leu
370 375 380

Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr
385 390 395 400

Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly
405 410 415

Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr
420 425 430

Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His
435 440 445

Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu
450 455 460

Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr
465 470 475 480

Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu
485 490 495

Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala
500 505 510

Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser
515 520 525

Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp
530 535 540

Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser
545 550 555 560

Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu
565 570 575

Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu
580 585 590

Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser
595 600 605

Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp
610 615 620

Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr
625 630 635 640

Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala
645 650 655

Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe
660 665

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<211> 908

<212> DNA

<213> Pasteurella multocida

<220>

<223> lgtc

<220>

<221> CDS

<222> (1)..(906)

<400> 106

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Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
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gtt gcg att aaa agc att ata aat cat aat gaa aaa ggt att tca ttt 96
Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
20 25 30

tat att ttt gat ttg ggt ata aag gat gaa aat aag aga aat att aat 144
Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
35 40 45

gat att gtt tct tct tat gga agt gaa gtc aac ttt att gct gtg aat 192
Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
50 55 60

gag aaa gaa ttt gag agt ttt cct gtt caa att agt tat att tct tta 240
Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
65 70 75 80

gca aca tat gca agg cta aaa gcg gca gag tat ttg ccg gat aat tta 288
Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
85 90 95

aat aaa att att tat tta gat gtt gat gtt ttg gtt ttt aac tca tta 336
Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
100 105 110

gaa atg tta tgg aat gtt gat gtt aat aat ttt ctt acc gca gcc tgt 384
Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
115 120 125

tat gat tct ttc atc gaa aat gaa aag tct gag cat aaa aaa tcg att	432
Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile	
130 135 140	
tca atg tca gat aag gaa tat tat ttt aat gca gga gta atg cta ttt	480
Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe	
145 150 155 160	
aat tta gat gaa tgg cgg aag atg gat gta ttc tca aga gct tta gac	528
Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp	
165 170 175	
ctg tta gct atg tat cct aat caa atg att tat cag gat caa gat ata	576
Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile	
180 185 190	
ttg aat atc ctt ttt agg aat aaa gtc tgt tat tta gat tgc aga ttt	624
Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe	
195 200 205	
aat ttc atg cca aat caa ctt gaa aga ata aaa caa tac cat aaa gga	672
Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly	
210 215 220	
aaa ttg agc aac tta cat tct tta gaa aaa aca acg atg cct gtc gtt	720
Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val	
225 230 235 240	
att tca cat tat tgt ggt cca gaa aaa gcg tgg cat gcg gat tgt aaa	768
Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys	
245 250 255	
cat ttt aat gta tat ttc tat cag aaa ata tta gca gaa ata acg aga	816
His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg	
260 265 270	
ggc acg gat aaa gaa cgc gta tta tct ata aaa act tat ctc aag gcc	864
Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala	
275 280 285	
ttg att aga agg att aga tat aaa ttc aaa tat caa gtc tat ta	908
Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr	
290 295 300	

<210> 107
<211> 302
<212> PRT
<213> Pasteurella multocida

<400> 107
Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
1 5 10 15
Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
20 25 30
Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
35 40 45
Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
50 55 60

Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
65 70 75 80

Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
85 90 95

Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
100 105 110

Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
115 120 125

Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
130 135 140

Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
145 150 155 160

Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp
165 170 175

Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile
180 185 190

Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
195 200 205

Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly
210 215 220

Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
225 230 235 240

Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
245 250 255

His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg
260 265 270

Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala
275 280 285

Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr
290 295 300

<210> 108
<211> 2054
<212> DNA
<213> Pasteurella multocida

<220>
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<220>
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<222> (1)...(2052)

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Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys
1 5 10 15

aaa gat gtg aaa gaa ggt caa gac ttc ttc cca tta act gtt aac tat	96
Lys Asp Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asn Tyr	
20 25 30	
caa gag cgt act tat gct gca ggc cgt att cct ggt ggc ttt ttc aaa	144
Gln Glu Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys	
35 40 45	
cgt gaa ggt cgt cct tct gaa ggc gaa act tta att gct cgt tta att	192
Arg Glu Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile	
50 55 60	
gac cgt cca att cgt cct ctt ttc cca gaa ggt ttt tat aac gaa atc	240
Asp Arg Pro Ile Arg Pro Leu Phe Pro Glu Gly Phe Tyr Asn Glu Ile	
65 70 75 80	
caa atc gtg gcg aca gtg gtg tct gtt aat ccg caa att tgt cca gat	288
Gln Ile Val Ala Thr Val Val Ser Val Asn Pro Gln Ile Cys Pro Asp	
85 90 95	
tta gtg gca atg atc ggt gca tct gcg gca ctt tct tta tca ggt gtg	336
Leu Val Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val	
100 105 110	
cca ttt aat ggc cct atc ggt gcg gca cgt gtt ggt ttt att gat gat	384
Pro Phe Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asp Asp	
115 120 125	
caa ttt gtg tta aac cca acc atg aac gag caa aaa caa agc cgt tta	432
Gln Phe Val Leu Asn Pro Thr Met Asn Glu Gln Lys Gln Ser Arg Leu	
130 135 140	
gac ttg gtt gtc gcg gga aca gat aaa gcg gtg tta atg gtg gaa tct	480
Asp Leu Val Val Ala Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser	
145 150 155 160	
gaa gcc gat gta tta acc gaa gaa caa atg tta gct gcg gtg gtg ttt	528
Glu Ala Asp Val Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe	
165 170 175	
ggt cat cag caa caa caa gtg gtg att gac gcg atc aaa gaa ttt acc	576
Gly His Gln Gln Gln Val Val Ile Asp Ala Ile Lys Glu Phe Thr	
180 185 190	
gca gaa gcc ggt aaa ccg cgt tgg gat tgg gtg gca cct gaa cca aat	624
Ala Glu Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn	
195 200 205	
acc gcg tta att gaa aaa gtg aaa gcg att gca gaa gcg cgt tta ggc	672
Thr Ala Leu Ile Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly	
210 215 220	
gaa gca tac cgt atc act gaa aaa caa gca cgt tat gaa caa att gat	720
Glu Ala Tyr Arg Ile Thr Glu Lys Gln Ala Arg Tyr Glu Gln Ile Asp	
225 230 235 240	
gcg att aaa gct gat gtg att gca caa atc aca gct gaa gta gca gaa	768
Ala Ile Lys Ala Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu	
245 250 255	
ggc gaa gac atc agt gaa ggg aaa att gtc gat att ttc acc gca ctt	816
Gly Glu Asp Ile Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu	
260 265 270	

gaa agc caa atc gta cgt agc cgt atc att gct ggt gaa cca cgt att	864
Glu Ser Gln Ile Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile	
275 280 285	
gat ggt cgt aca gtc gat act gtt cgt gca tta gat att tgt act ggt	912
Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly	
290 295 300	
gtt tta cca cgt aca cac ggt tct gcg att ttc acc cgt ggt gaa aca	960
Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr	
305 310 315 320	
cag gcg tta gct gtc gcg aca tta ggt aca gaa cgt gat gca caa att	1008
Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile	
325 330 335	
att gat gaa tta aca ggt gag cgt tca gat cac ttc tta ttc cac tac	1056
Ile Asp Glu Leu Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr	
340 345 350	
aac ttc ccg cca tat tct gtg ggt gaa acc ggt atg att ggt tca cca	1104
Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro	
355 360 365	
aaa cgt cgt gaa att ggt cat ggt cgt tta gcg aaa cgc ggt gta gct	1152
Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala	
370 375 380	
gca gtg atg cca aca ctt gcc gag ttc ccg tat gtg gta cgt gtt gtc	1200
Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val	
385 390 395 400	
tct gaa atc aca gaa tca aat ggt tct tct atg gca tcg gtt tgt	1248
Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Met Ala Ser Val Cys	
405 410 415	
ggg gcg tct tta gca tta atg gat gcg ggt gta cca att aaa gcg gcg	1296
Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala	
420 425 430	
gtt gca ggt att gca atg ggc tta gtc aaa gaa gac gaa aaa ttt gtg	1344
Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val	
435 440 445	
gtg ctt tca gac atc tta ggt gat gaa gat cac tta ggt gac atg gac	1392
Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp	
450 455 460	
ttc aaa gtc gcg ggt aca cgt acg ggt gtc acg gca tta caa atg gat	1440
Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp	
465 470 475 480	
atc aaa atc gaa ggt atc aca gca gaa atc atg caa att gcg tta aac	1488
Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn	
485 490 495	
caa gcg aaa agc gca cgt tta cac att tta ggt gtg atg gag caa gcg	1536
Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala	
500 505 510	
atc cca gcg cca cgt gcg gat att tct gat ttt gca ccg cgt att tac	1584
Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr	
515 520 525	

act atg aaa att gat ccg aag aaa atc aaa gat gtg atc ggt aaa ggt	1632
Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly	
530 535 540	
ggt gca acc att cgt gcc tta aca gaa gaa aca ggt acc tca att gat	1680
Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp	
545 550 555 560	
atc gat gat gat ggt acg gtg aag att gct gcg gtt gat ggc aat tca	1728
Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser	
565 570 575	
gca aaa gag gtg atg gcg cgt att gaa gat att act gca gaa gtt gaa	1776
Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu	
580 585 590	
gcg ggt gca gtg tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt	1824
Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly	
595 600 605	
gcc ttc gtt tct atc gta ggt aac aaa gaa ggc tta gtg cat att tct	1872
Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser	
610 615 620	
caa atc gcg gaa gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg	1920
Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val	
625 630 635 640	
ggg caa gaa gtg act gtt aaa gtg gtt gag att gat cgt caa ggt cgt	1968
Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg	
645 650 655	
att cgt tta acc atg aaa gaa gtt gca cca aag caa gaa cac gtt gat	2016
Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp	
660 665 670	
tct gtt gtc gca gac gtt gcc gca gaa gaa aac gca ta	2054
Ser Val Val Ala Asp Val Ala Ala Glu Glu Asn Ala	
675 680	

<210> 109

<211> 684

<212> PRT

<213> Pasteurella multocida

<400> 109

Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys

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5

10

15

Lys Asp Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asn Tyr

20

25

30

Gln Glu Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys

35

40

45

Arg Glu Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile

50

55

60

Asp Arg Pro Ile Arg Pro Leu Phe Pro Glu Gly Phe Tyr Asn Glu Ile

65

70

75

80

Gln Ile Val Ala Thr Val Val Ser Val Asn Pro Gln Ile Cys Pro Asp

85

90

95

Leu Val Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val
100 105 110

Pro Phe Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asp Asp
115 120 125

Gln Phe Val Leu Asn Pro Thr Met Asn Glu Gln Lys Gln Ser Arg Leu
130 135 140

Asp Leu Val Val Ala Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser
145 150 155 160

Glu Ala Asp Val Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe
165 170 175

Gly His Gln Gln Gln Val Val Ile Asp Ala Ile Lys Glu Phe Thr
180 185 190

Ala Glu Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn
195 200 205

Thr Ala Leu Ile Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly
210 215 220

Glu Ala Tyr Arg Ile Thr Glu Lys Gln Ala Arg Tyr Glu Gln Ile Asp
225 230 235 240

Ala Ile Lys Ala Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu
245 250 255

Gly Glu Asp Ile Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu
260 265 270

Glu Ser Gln Ile Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile
275 280 285

Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly
290 295 300

Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr
305 310 315 320

Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile
325 330 335

Ile Asp Glu Leu Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr
340 345 350

Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro
355 360 365

Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala
370 375 380

Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val
385 390 395 400

Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys
405 410 415

Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala

420	425	430
Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val		
435	440	445
Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp		
450	455	460
Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp		
465	470	475
Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn		
485	490	495
Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala		
500	505	510
Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr		
515	520	525
Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly		
530	535	540
Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp		
545	550	555
Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser		
565	570	575
Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu		
580	585	590
Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly		
595	600	605
Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser		
610	615	620
Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val		
625	630	635
Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg		
645	650	655
Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp		
660	665	670
Ser Val Val Ala Asp Val Ala Ala Glu Glu Asn Ala		
675	680	

<210> 110
<211> 1514
<212> DNA
<213> *Pasteurella multocida*

<220>
<223> *purF*

<220>
<221> CDS
<222> (1)..(1512)

<400> 110
atg tgt ggt att gtt ggt att gtt agc caa agc ccc gtt aac caa tca 48
Met Cys Gly Ile Val Gly Ile Val Ser Gln Ser Pro Val Asn Gln Ser
1 5 10 15

att tat gat gcg tta acc tta ttg caa cac cgc ggg caa gac gcc gcc 96
Ile Tyr Asp Ala Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala
20 25 30

ggg att gta acc gta gat gat gaa aac cga ttc cgc ttg cgt aaa gcg 144
Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala
35 40 45

aac ggg tta gtc agc gat gta ttt gaa caa gtt cat atg tta cgt tta 192
Asn Gly Leu Val Ser Asp Val Phe Glu Gln Val His Met Leu Arg Leu
50 55 60

caa ggc aat gct ggc att gga cat gtt cgt tat cct acg gct ggg agc 240
Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser
65 70 75 80

tca agt gtc tct gaa gcg caa cct ttt tat gta aat tcg cct tat ggc 288
Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly
85 90 95

tta acc tta gtg cat aat ggt aac ttg acc aat tca agt gaa tta aaa 336
Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys
100 105 110

gaa aag tta ttt cgt ctc gca cgt cgc cat gta aat acc aat tca gat 384
Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp
115 120 125

tct gaa tta tta ctc aat atc tta gcc aat cac ctt gat cac ttc gaa 432
Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu
130 135 140

aaa tac caa tta gat ccg caa gat gta ttc agt gct gtc aaa caa acg 480
Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr
145 150 155 160

cat cag gat att cgt ggt gct tat gct tgt atc gcc atg att att ggt 528
His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly
165 170 175

cat ggt atg gtc gcg ttt cgt gat ccg aac ggt atc cgt ccg tta gtg 576
His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val
180 185 190

tta ggg aaa cgc gag gaa aat ggc aaa aca gag tat atg ttt gcc tcc 624
Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser
195 200 205

gaa agt atc gca tta gat aca gtg ggt ttt gag ttt gta cga gat gta 672
Glu Ser Ile Ala Leu Asp Thr Val Gly Phe Glu Phe Val Arg Asp Val
210 215 220

caa ccc ggc gaa gcg att tat gtc acg ttt gaa ggg gaa atg tat gct 720
Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala
225 230 235 240

cag caa tgc gca gac aaa cca aca aca cct tgt att ttt gaa tac 768
Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr

	245	250	255	
gtc tat ttt gca cgt cca gac tct tgc atc gat ggg gtt tct gtt tat				816
Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr				
260	265	270		
gct gcc cgt gtt cat atg gga caa cgt tta ggt gaa aaa att gca cgg				864
Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg				
275	280	285		
gaa tgg gcg gat gtg gat gat att gat gtg gtc att cct gtg cct gaa				912
Glu Trp Ala Asp Val Asp Ile Asp Val Val Ile Pro Val Pro Glu				
290	295	300		
acc tct aac gat att gct tta cgt att gcg cgc gtg tta aat aaa ccg				960
Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro				
305	310	315	320	
tat cgt caa ggt ttt gtg aaa aat cgc tat gta gga cgt acg ttt att				1008
Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile				
325	330	335		
atg ccg ggg cag gca ttg cga gtc agt tct gtt aga cgt aaa ctc aat				1056
Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn				
340	345	350		
acc att gct tca gaa ttt aaa gat aag aat gtg tta tta gtt gac gac				1104
Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp				
355	360	365		
tcg att gta cgt ggt acc acg tct gaa caa att gtc gaa atg gcg aga				1152
Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg				
370	375	380		
gcg gca ggt gcg aag aaa att tat ttt gcc tct gct gca cca gaa att				1200
Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile				
385	390	395	400	
cgt tat cca aat gtg tat ggt att gat atg cca acc aaa aat gaa ttg				1248
Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu				
405	410	415		
atc gct tat ggt cgt gat gta gat gaa att gct aac tta att ggt gtg				1296
Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val				
420	425	430		
gat aaa ttg att ttc caa gat ttg gat gcg tta act ggt tct gtg caa				1344
Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln				
435	440	445		
caa gaa aat cca agt att caa gac ttt gat tgt tcg gtg ttt aca ggg				1392
Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly				
450	455	460		
gtt tat gtg acg ggc gat att aca cct gaa tat ctg gat aat att gca				1440
Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala				
465	470	475	480	
gaa cag cgt aat gat atc gcc aag aaa aag cgt gaa aaa gat gct acc				1488
Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr				
485	490	495		
aat ctt gaa atg cac aat gaa aaa ta				1514

Asn Leu Glu Met His Asn Glu Lys
500

<210> 111
<211> 504
<212> PRT
<213> Pasteurella multocida

<400> 111
Met Cys Gly Ile Val Gly Ile Val Ser Gln Ser Pro Val Asn Gln Ser
1 5 10 15
Ile Tyr Asp Ala Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala
20 25 30
Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala
35 40 45
Asn Gly Leu Val Ser Asp Val Phe Glu Gln Val His Met Leu Arg Leu
50 55 60
Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser
65 70 75 80
Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly
85 90 95
Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys
100 105 110
Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp
115 120 125
Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu
130 135 140
Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr
145 150 155 160
His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly
165 170 175
His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val
180 185 190
Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser
195 200 205
Glu Ser Ile Ala Leu Asp Thr Val Gly Phe Glu Phe Val Arg Asp Val
210 215 220
Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala
225 230 235 240
Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr
245 250 255
Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr
260 265 270
Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg
275 280 285

Glu Trp Ala Asp Val Asp Asp Ile Asp Val Val Ile Pro Val Pro Glu
290 295 300

Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro
305 310 315 320

Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile
325 330 335

Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn
340 345 350

Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp
355 360 365

Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg
370 375 380

Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile
385 390 395 400

Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu
405 410 415

Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val
420 425 430

Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln
435 440 445

Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly
450 455 460

Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala
465 470 475 480

Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr
485 490 495

Asn Leu Glu Met His Asn Glu Lys
500

<210> 112

<211> 989

<212> DNA

<213> *Pasteurella multocida*

<220>

<223> rci

<220>

<221> CDS

<222> (1)..(987)

<400> 112

atg gca aca ata aga aaa cgt ggt aac tca tat cgt gct gag ata agc 48
Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser
1 5 10 15

aaa aac gga gta agg aaa tca gca aca ttt aag act aaa tca gaa gct 96
Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala
20 25 30

aat gcg tgg gct gtt gac gag gag aga aaa tta gct gat ttg gca aaa	144
Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys	
35 40 45	
ggt atc gct cca gat att att ttt aga gat gta ata gaa cgc tat caa	192
Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln	
50 55 60	
aat gaa gtg tct ata act aaa aaa ggc gcg cga aat gaa att ata aga	240
Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg	
65 70 75 80	
tta aac cgc ttt tta aga tat gat att tct aat ctg tat att cgt gat	288
Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp	
85 90 95	
tta aga aaa gaa gat ttt gag gag tgg atc aga att cgc cta acc gaa	336
Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu	
100 105 110	
gta tcg gat gct agc gtt aga cgt gag ctt gtt act ata tcg tca gtg	384
Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val	
115 120 125	
ctg aca aca gca ata aat aag tgg gga tat att tca agg cat cca atg	432
Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met	
130 135 140	
act ggt att gaa aaa cca aaa aac tcg gca gaa aga aaa gaa cga tat	480
Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr	
145 150 155 160	
tca gaa cag gac att aaa aca ata tta gaa aca gct aga tat tgt gaa	528
Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu	
165 170 175	
gat aaa cta ccc ata aca ctc aaa caa aga gta gca att gca atg tta	576
Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu	
180 185 190	
ttt gct att gaa acc gct atg cgt gct ggt gag att gct agt ata aaa	624
Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys	
195 200 205	
tgg gat aat gtt ttt ctt gaa aag aga ata gta cat tta ccg aca act	672
Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr	
210 215 220	
aaa aac ggg cac tct aga gat gtg ccg ctt tcg caa aga gct gtt gcg	720
Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala	
225 230 235 240	
cta att tta aaa atg aaa gag gta gaa aat gga gat ctt gtg ttt cag	768
Leu Ile Leu Lys Met Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln	
245 250 255	
acc acg cct gaa tca tta agc acc acg ttt aga gtg tta aag aaa gag	816
Thr Thr Pro Glu Ser Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu	
260 265 270	
tgt gga ctt gaa cat ctc cat ttt cat gat acg aga agg gaa gcg ttg	864
Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu	
275 280 285	

acg aga tta tct aag aaa gta gat gta atg act cta gcc aaa att agc	912
Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser	
290 295 300	
gga cat aga gat tta aga att tta caa aac aca tat tac gca ccg aat	960
Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn	
305 310 315 320	
atg agt gaa gtg gca aac ttg ttg gat ta	989
Met Ser Glu Val Ala Asn Leu Leu Asp	
325	
<210> 113	
<211> 329	
<212> PRT	
<213> Pasteurella multocida	
<400> 113	
Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser	
1 5 10 15	
Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala	
20 25 30	
Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys	
35 40 45	
Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln	
50 55 60	
Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg	
65 70 75 80	
Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp	
85 90 95	
Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu	
100 105 110	
Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val	
115 120 125	
Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met	
130 135 140	
Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr	
145 150 155 160	
Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu	
165 170 175	
Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu	
180 185 190	
Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys	
195 200 205	
Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr	
210 215 220	
Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala	
225 230 235 240	

Leu Ile Leu Lys Met Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln
245 250 255

Thr Thr Pro Glu Ser Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu
260 265 270

Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu
275 280 285

Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser
290 295 300

Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn
305 310 315 320

Met Ser Glu Val Ala Asn Leu Leu Asp
325

<210> 114
<211> 1190
<212> DNA
<213> Pasteurella multocida

<220>
<223> sopE

<220>
<221> CDS
<222> (1)..(1188)

<400> 114
atg tct gaa gaa tat cta cat ggt gtc aaa gtc aca gaa atc aat caa 48
Met Ser Glu Glu Tyr Leu His Gly Val Lys Val Thr Glu Ile Asn Gln
1 5 10 15

gca att cgc aca att caa agt cta tca acc gca gtc atc ggt att gtc 96
Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val
20 25 30

tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat gaa ccc 144
Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro
35 40 45

gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga aaa caa 192
Val Leu Ile Thr Asn Val Ala Ala Ile Gly Lys Ala Gly Lys Gln
50 55 60

ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc aat tgc 240
Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys
65 70 75 80

aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac gaa gaa 288
Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu
85 90 95

aca aaa gca agt gaa atg aac acg gca att att ggc aca atc aca gaa 336
Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu
100 105 110

gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa aac aaa 384
Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys
115 120 125

ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac aca aaa	432
Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys	
130 135 140	
gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac gca ttt	480
Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe	
145 150 155 160	
gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg gtg caa	528
Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln	
165 170 175	
tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg ggc gat	576
Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp	
180 185 190	
ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac tat gcc	624
Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala	
195 200 205	
gtc act cgt gcg gca atg cgt gca tat ctt gat aaa gaa cag ggc	672
Val Thr Arg Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly	
210 215 220	
tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc ggt gtc	720
Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val	
225 230 235 240	
aca caa cca ctc tat ttt gac att aac gac agc tcg act gat gtg aac	768
Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn	
245 250 255	
tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat ggc ttt	816
Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe	
260 265 270	
cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc aag ttt	864
Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe	
275 280 285	
gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att gca ggg	912
Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly	
290 295 300	
gcg ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta gtg aaa	960
Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys	
305 310 315 320	
gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc aca aaa	1008
Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys	
325 330 335	
ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt aac agt	1056
Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser	
340 345 350	
gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat tat cac	1104
Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His	
355 360 365	
cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att tct gat	1152
Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp	
370 375 380	

gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg ta 1190
Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
385 390 395

<210> 115
<211> 396
<212> PRT
<213> Pasteurella multocida

<400> 115
Met Ser Glu Glu Tyr Leu His Gly Val Lys Val Thr Glu Ile Asn Gln 15
1 5 10 15

Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val 20 25 30

Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro 35 40 45

Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly Lys Gln 50 55 60

Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys 65 70 75 80

Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu 85 90 95

Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu 100 105 110

Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys 115 120 125

Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys 130 135 140

Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe 145 150 155 160

Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln 165 170 175

Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp 180 185 190

Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala 195 200 205

Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly 210 215 220

Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val 225 230 235 240

Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn 245 250 255

Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe 260 265 270

Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe

275	280	285
Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly		
290	295	300
Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys		
305	310	315
Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys		
325	330	335
Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser		
340	345	350
Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His		
355	360	365
Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp		
370	375	380
Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser		
385	390	395
<210> 116		
<211> 2204		
<212> DNA		
<213> Pasteurella multocida		
<220>		
<223> unkK		
<220>		
<221> CDS		
<222> (1)...(2202)		
<400> 116		
atg aat aaa aat cgc tat aaa ctc att ttt agt aaa act aaa ggc tgt		48
Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys		
1	5	10
		15
ctt gta cct gtt gct gaa acg att aat tct gca gta gga aat gcc tca		96
Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser		
20	25	30
tca aaa gac gtt tct gac acc gag ata agt gct tct caa cca gcg ctc		144
Ser Lys Asp Val Ser Asp Thr Glu Ile Ser Ala Ser Gln Pro Ala Leu		
35	40	45
aac tcg ccg ctt tcg acc ctt tct gta tta gtc aaa acc gca ttt aat		192
Asn Ser Pro Leu Ser Thr Leu Ser Val Leu Val Lys Thr Ala Phe Asn		
50	55	60
ccg gtt tca aca ttg atg tcg ttg act tgg aaa gaa tac gcc gtt tta		240
Pro Val Ser Thr Leu Met Ser Leu Thr Trp Lys Glu Tyr Ala Val Leu		
65	70	75
		80
tta tta agt gtg gtg tct ttt cct ctt atg gca caa gcc tct gat aca		288
Leu Leu Ser Val Val Ser Phe Pro Leu Met Ala Gln Ala Ser Asp Thr		
85	90	95
gat tca gtg gta caa aga aaa cct gaa tta act gat gtg acg aat agc		336
Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser		

100	105	110	
aac agc tat cat gtg gaa tta gat aga gag cat cat aaa ggg gag cat			384
Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His			
115	120	125	
caa aca aaa atc aaa cat act gag aat aat gtc atc att gtt gat att			432
Gln Thr Lys Ile Lys His Thr Glu Asn Asn Val Ile Ile Val Asp Ile			
130	135	140	
gca aaa cca aaccaa aag ggc att tca gat aac cgt ttt aaa cac ttc			480
Ala Lys Pro Asn Gln Lys Gly Ile Ser Asp Asn Arg Phe Lys His Phe			
145	150	155	160
aac atc cca aat ggg gcg gta ttt aac aat agc gcc aag gaa aaa cgc			528
Asn Ile Pro Asn Gly Ala Val Phe Asn Asn Ser Ala Lys Glu Lys Arg			
165	170	175	
tca cag tta gtg ggg tat ttg cca ggt aac cag aat tta acg gaa ggt			576
Ser Gln Leu Val Gly Tyr Leu Pro Gly Asn Gln Asn Leu Thr Glu Gly			
180	185	190	
agt gaa gca aaa gcg atc tta aat cag gtg act gga ccg gat gcc agt			624
Ser Glu Ala Lys Ala Ile Leu Asn Gln Val Thr Gly Pro Asp Ala Ser			
195	200	205	
aaa att gaa ggc gcc ctt gaa att tta ggg caa aaa gcc gat ttg gtg			672
Lys Ile Glu Gly Ala Leu Glu Ile Leu Gly Gln Lys Ala Asp Leu Val			
210	215	220	
att gcg aac caa aat ggc att gtg ctt aat ggg gta aaa acc att aat			720
Ile Ala Asn Gln Asn Gly Ile Val Leu Asn Gly Val Lys Thr Ile Asn			
225	230	235	240
gcc aat cgt ttt gtg gca aca acc agt agt acc att gat cct gag caa			768
Ala Asn Arg Phe Val Ala Thr Thr Ser Ser Thr Ile Asp Pro Glu Gln			
245	250	255	
atg cag tta aat gtc acg caa ggt aca gtg aca att ggg gtg gat gga			816
Met Gln Leu Asn Val Thr Gln Gly Thr Val Thr Ile Gly Val Asp Gly			
260	265	270	
ttt gcc aca gat ggc tta cct tat ttg gat atc att gcc aaa aag att			864
Phe Ala Thr Asp Gly Leu Pro Tyr Leu Asp Ile Ile Ala Lys Lys Ile			
275	280	285	
gaa caa aaa caa gcg att aca aaa gaa aga aca gga aat tcc gaa acc			912
Glu Gln Lys Gln Ala Ile Thr Lys Glu Arg Thr Gly Asn Ser Glu Thr			
290	295	300	
gat atc act ttt gtc gca ggt aac agt aaa tat gat tta aag aca cat			960
Asp Ile Thr Phe Val Ala Gly Asn Ser Lys Tyr Asp Leu Lys Thr His			
305	310	315	320
caa gtg aca gaa aag cat acc gct gag gca caa ggt gaa att gcg att			1008
Gln Val Thr Glu Lys His Thr Ala Glu Ala Gln Gly Glu Ile Ala Ile			
325	330	335	
agc ggt gcg agt acc ggt gca atg tac ggt aaa aat atc aaa tta atc			1056
Ser Gly Ala Ser Thr Gly Ala Met Tyr Gly Lys Asn Ile Lys Leu Ile			
340	345	350	
gta acg gat aaa ggc gct ggg gta aaa cat gat ggc att att tta tct			1104

Val Thr Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser			
355	360	365	
gag gcg gat att caa att gaa acc cat gag ggc gat gtt gaa tta ggc			1152
Glu Ala Asp Ile Gln Ile Glu Thr His Glu Gly Asp Val Glu Leu Gly			
370	375	380	
aat aca aaa aat aat cag aat gag aat tat gcc aaa gct cat gcg gaa			1200
Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu			
385	390	395	400
ggg aat ttt acg gtt aaa ggc ggt aag cac gtt att att ggt aag gaa			1248
Gly Asn Phe Thr Val Lys Gly Gly Lys His Val Ile Ile Gly Lys Glu			
405	410	415	
gtt aaa gcc aac aaa gcg gtc gat att caa gca caa gaa aca aca gta			1296
Val Lys Ala Asn Lys Ala Val Asp Ile Gln Ala Gln Glu Thr Thr Val			
420	425	430	
aga caa aat gcg aaa tta act gcc aaa acg agt gcc aaa att aca gca			1344
Arg Gln Asn Ala Lys Leu Thr Ala Lys Thr Ser Ala Lys Ile Thr Ala			
435	440	445	
agt aag agt gtg aat ctt gaa gat aac gcg aaa ctt att gct aat gag			1392
Ser Lys Ser Val Asn Leu Glu Asp Asn Ala Lys Leu Ile Ala Asn Glu			
450	455	460	
ctg agc aca aca acc aat aaa tta acc aat aaa ggt agc att tac ggc			1440
Leu Ser Thr Thr Asn Lys Leu Thr Asn Lys Gly Ser Ile Tyr Gly			
465	470	475	480
aag aaa gtg acg cta gat gct gat aat tta gtc aat agt aaa gaa atc			1488
Lys Lys Val Thr Leu Asp Ala Asp Asn Leu Val Asn Ser Lys Glu Ile			
485	490	495	
tat gcg tct agc gaa ctt gat att caa acc aaa ggt cgt gat ctt tta			1536
Tyr Ala Ser Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu			
500	505	510	
ctt gag gat ggg gtt aat caa cca ctg agt ttc tta aaa ggc gct tca			1584
Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser			
515	520	525	
ttg tta gcg ccg ggg ttt gtc aac act ggg cta att cac agt aac ggt			1632
Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly			
530	535	540	
aat gcc aag ctc act ttt aaa gat gac acc agt ttt gtg act gaa gga			1680
Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly			
545	550	555	560
aat aac ttt atc aca gca aaa gac aac tta gaa atc acg gca aaa aat			1728
Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn			
565	570	575	
gtt caa att gat caa gcg aaa aat att caa tta aac gcg aat atc acg			1776
Val Gln Ile Asp Gln Ala Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr			
580	585	590	
atc aat acc aag tct ggt ttt gtg aat tac ggt acc tta gca agt gct			1824
Ile Asn Thr Lys Ser Gly Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala			
595	600	605	

caa aat tta acg att aat acc gaa caa ggc agc att tat aac ata ggc Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly 610 615 620	1872
ggt atc ttg ggg gcg ggt aaa agt ttg aat ctg agc gcg aaa aga gga Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly 625 630 635 640	1920
gaa aac caa gga gga tat ctt att aat caa ggt aag agt cta ctc cat Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His 645 650 655	1968
tct gaa ggc gcc atg aac ctc aca gcg gat cgc acg gtg tac aat tta Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu 660 665 670	2016
ggg aat att ttt gct aaa ggt gac gcg acg atc aat gca aac gcg tta Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu 675 680 685	2064
att aat gat gtt act ctc aca ggt cgt ctt gag tat caa gat ctg aaa Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys 690 695 700	2112
aaa gat tat acg cgt tat tat cgt atc aat gaa acg gca aaa cat ggt Lys Asp Tyr Thr Arg Tyr Arg Ile Asn Glu Thr Ala Lys His Gly 705 710 715 720	2160
tgg cat aat aac ttc tat gaa tta aac gtc gac aga gtt tct tg Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser 725 730	2204

<210> 117

<211> 734

<212> PRT

<213> Pasteurella multocida

<400> 117

Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys 1 5 10 15
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Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser 20 25 30

Ser Lys Asp Val Ser Asp Thr Glu Ile Ser Ala Ser Gln Pro Ala Leu 35 40 45

Asn Ser Pro Leu Ser Thr Leu Ser Val Leu Val Lys Thr Ala Phe Asn 50 55 60

Pro Val Ser Thr Leu Met Ser Leu Thr Trp Lys Glu Tyr Ala Val Leu 65 70 75 80
--

Leu Leu Ser Val Val Ser Phe Pro Leu Met Ala Gln Ala Ser Asp Thr 85 90 95

Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser 100 105 110
--

Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His 115 120 125
--

Gln Thr Lys Ile Lys His Thr Glu Asn Asn Val Ile Ile Val Asp Ile
130 135 140

Ala Lys Pro Asn Gln Lys Gly Ile Ser Asp Asn Arg Phe Lys His Phe
145 150 155 160

Asn Ile Pro Asn Gly Ala Val Phe Asn Asn Ser Ala Lys Glu Lys Arg
165 170 175

Ser Gln Leu Val Gly Tyr Leu Pro Gly Asn Gln Asn Leu Thr Glu Gly
180 185 190

Ser Glu Ala Lys Ala Ile Leu Asn Gln Val Thr Gly Pro Asp Ala Ser
195 200 205

Lys Ile Glu Gly Ala Leu Glu Ile Leu Gly Gln Lys Ala Asp Leu Val
210 215 220

Ile Ala Asn Gln Asn Gly Ile Val Leu Asn Gly Val Lys Thr Ile Asn
225 230 235 240

Ala Asn Arg Phe Val Ala Thr Thr Ser Ser Thr Ile Asp Pro Glu Gln
245 250 255

Met Gln Leu Asn Val Thr Gln Gly Thr Val Thr Ile Gly Val Asp Gly
260 265 270

Phe Ala Thr Asp Gly Leu Pro Tyr Leu Asp Ile Ile Ala Lys Lys Ile
275 280 285

Glu Gln Lys Gln Ala Ile Thr Lys Glu Arg Thr Gly Asn Ser Glu Thr
290 295 300

Asp Ile Thr Phe Val Ala Gly Asn Ser Lys Tyr Asp Leu Lys Thr His
305 310 315 320

Gln Val Thr Glu Lys His Thr Ala Glu Ala Gln Gly Glu Ile Ala Ile
325 330 335

Ser Gly Ala Ser Thr Gly Ala Met Tyr Gly Lys Asn Ile Lys Leu Ile
340 345 350

Val Thr Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser
355 360 365

Glu Ala Asp Ile Gln Ile Glu Thr His Glu Gly Asp Val Glu Leu Gly
370 375 380

Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu
385 390 395 400

Gly Asn Phe Thr Val Lys Gly Gly Lys His Val Ile Ile Gly Lys Glu
405 410 415

Val Lys Ala Asn Lys Ala Val Asp Ile Gln Ala Gln Glu Thr Thr Val
420 425 430

Arg Gln Asn Ala Lys Leu Thr Ala Lys Thr Ser Ala Lys Ile Thr Ala
435 440 445

Ser Lys Ser Val Asn Leu Glu Asp Asn Ala Lys Leu Ile Ala Asn Glu
450 455 460

Leu Ser Thr Thr Asn Lys Leu Thr Asn Lys Gly Ser Ile Tyr Gly
465 470 475 480

Lys Lys Val Thr Leu Asp Ala Asp Asn Leu Val Asn Ser Lys Glu Ile
485 490 495

Tyr Ala Ser Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu
500 505 510

Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser
515 520 525

Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly
530 535 540

Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly
545 550 555 560

Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn
565 570 575

Val Gln Ile Asp Gln Ala Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr
580 585 590

Ile Asn Thr Lys Ser Gly Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala
595 600 605

Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly
610 615 620

Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly
625 630 635 640

Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His
645 650 655

Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu
660 665 670

Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu
675 680 685

Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys
690 695 700

Lys Asp Tyr Thr Arg Tyr Tyr Arg Ile Asn Glu Thr Ala Lys His Gly
705 710 715 720

Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser
725 730

<210> 118
<211> 251
<212> DNA
<213> *Pasteurella multocida*

<220>
<223> unkO

<220>
<221> CDS
<222> (1)..(249)

<400> 118
atg aaa att act att aca cga aat cat cca gaa gta ttt caa gaa tcc 48
Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
1 5 10 15

gct cgt tta gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca 96
Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
20 25 30

tta aca ttg gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt 144
Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
35 40 45

gag gag gaa agc aaa agg gga cat agt att aag gtt gta tta aaa gga 192
Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly
50 55 60

agt cac gaa gtt att aag tca gag gtg aat aca aat gaa aaa aat cat 240
Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His
65 70 75 80

tgt aat cat ta 251
Cys Asn His

<210> 119
<211> 83
<212> PRT
<213> Pasteurella multocida

<400> 119
Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser 15
1 5 10 15

Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
20 25 30

Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
35 40 45

Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly
50 55 60

Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His
65 70 75 80

Cys Asn His

<210> 120
<211> 548
<212> DNA
<213> Pasteurella multocida

<220>
<223> unkP

<220>
<221> CDS
<222> (1)...(546)

<400> 120

atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att tca	48
Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser	
1 5 10 15	
aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat ttt	96
Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe	
20 25 30	
gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa ggc	144
Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly	
35 40 45	
atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta cgc	192
Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg	
50 55 60	
acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc act	240
Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr	
65 70 75 80	
gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca gtg	288
Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val	
85 90 95	
gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca atc	336
Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile	
100 105 110	
aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc ggt	384
Asn Ala Lys Trp Arg Asp Tyr Thr Lys Gly Tyr Leu Ile Gly Gly	
115 120 125	
aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa gat	432
Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp	
130 135 140	
gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc gaa	480
Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu	
145 150 155 160	
cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat ttt	528
Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe	
165 170 175	
tca aat cgt tta gca tcg ta	548
Ser Asn Arg Leu Ala Ser	
180	
<210> 121	
<211> 182	
<212> PRT	
<213> Pasteurella multocida	
<400> 121	
Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser	
1 5 10 15	
Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe	
20 25 30	
Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly	
35 40 45	

Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg
50 55 60

Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr
65 70 75 80

Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val
85 90 95

Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile
100 105 110

Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly
115 120 125

Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp
130 135 140

Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu
145 150 155 160

Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe
165 170 175

Ser Asn Arg Leu Ala Ser
180

<210> 122
<211> 69
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> *apvA-ori1*

<220>
<221> CDS
<222> (1)..(69)

<400> 122
atg ttt tat gtc atg ctt gcc aat agg acg tct ata att tca tca atc 48
Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile
1 5 10 15

gat aag ttt aag ata ctt agc 69
Asp Lys Phe Lys Ile Leu Ser
20

<210> 123
<211> 23
<212> PRT
<213> *Actinobacillus pleuropneumoniae*

<400> 123
Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile
1 5 10 15

Asp Lys Phe Lys Ile Leu Ser
20

<210> 124
<211> 64
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> *apvA-or2*

<220>
<221> CDS
<222> (3)..(62)

<400> 124 47
ag cta agt atc tta aac tta tcg att gat gaa att ata gac gtc cta
Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu
1 5 10 15

ttg gca agc atg aca ta 64
Leu Ala Ser Met Thr
20

<210> 125
<211> 20
<212> PRT
<213> *Actinobacillus pleuropneumoniae*

<400> 125
Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu Leu
1 5 10 15

Ala Ser Met Thr
20

<210> 126
<211> 653
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> *apvB*

<220>
<221> CDS
<222> (1)..(651)

<400> 126 48
tta att agc ttt cct ttt att act ttt gca agt aat gtt aat gga gcc
Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala
1 5 10 15

gaa att gga ttg gga gga gcc cgt gag agt aat tac tat tct aaa 96
Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys
20 25 30

cat aaa gta gca aca aat ccc ttt tta gca ctt gat ctt tct tta ggt 144
His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly
35 40 45

aat ttt tat atg aga ggg act gca gga att agc gaa ata gga tat gaa 192
Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu
50 55 60

caa tct ttc act gac aat ttc agc gta tca ctg ttt gtt aac cca ttt	240
Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe	
65 70 75 80	
gat ggt ttt tca att aaa gga aaa gac ttg tta cct gga tat caa agt	288
Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser	
85 90 95	
att caa act cgc aaa act caa ttt gcc ttt ggt tgg gga tta aat tat	336
Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr	
100 105 110	
aat ttg gga ggt tta ttc ggc tta aat gat act ttt ata tcc ttg gaa	384
Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu	
115 120 125	
gga aaa agc gga aaa cgt ggt gcg agt agt aat gtc agc tta ctt aaa	432
Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys	
130 135 140	
tcg ttt aat atg acg aaa aat tgg aaa gtt tca cca tat att ggc tca	480
Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser	
145 150 155 160	
agt tat tat tca tct aaa tat aca gat tat tac ttt ggt att aaa caa	528
Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln	
165 170 175	
tcc gaa tta ggt aat aaa att aca tcc gta tat aaa cct aaa gca gct	576
Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala	
180 185 190	
tat gca aca cac ata ggt att aat act gat tat gct ttc acg aac aat	624
Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn	
195 200 205	
ctt ggc atg ggt tta tct gtc ggt tgg at	653
Leu Gly Met Gly Leu Ser Val Gly Trp	
210 215	

<210> 127

<211> 217

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 127

Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala

1

5

10

15

Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys

20

25

30

His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly

35

40

45

Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu

50

55

60

Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe

65

70

75

80

Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser

85

90

95

Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr
100 105 110

Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu
115 120 125

Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys
130 135 140

Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser
145 150 155 160

Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln
165 170 175

Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala
180 185 190

Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn
195 200 205

Leu Gly Met Gly Leu Ser Val Gly Trp
210 215

<210> 128

<211> 242

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> apvC

<220>

<221> CDS

<222> (1)..(240)

<400> 128

atg tgg cgg atg gga gat ttt atg tct aaa aaa gag agg ctg aat gat 48
Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp
1 5 10 15

atg gct cgc cag att tta tca gcg gcg gag ttg ctc att gca aag gaa 96
Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Leu Ile Ala Lys Glu
20 25 30

ggt ttg caa aat tta tcg atg agg aaa atc gca agt gaa gcc ggt atc 144
Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
35 40 45

gca aca ggc acg ctt tat ctc tat ttc aaa acg aaa gac gag tta ctg 192
Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
50 55 60

gat tgt ttg gcg gaa caa tta cat gaa cga tat tat cgt tat ctg aat 240
Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
65 70 75 80

at 242

<210> 129
<211> 80
<212> PRT
<213> *Actinobacillus pleuropneumoniae*

<400> 129
Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp
1 5 10 15

Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Leu Ile Ala Lys Glu
20 25 30

Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
35 40 45

Ala Thr Gly Thr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
50 55 60

Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
65 70 75 80

<210> 130
<211> 527
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> *apvD*

<220>
<221> CDS
<222> (1)..(525)

<400> 130
aat att caa aaa aca gtt att gct agc ggc aca ttg caa gcg act gaa 48
Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu
1 5 10 15

caa gta gat att ggt gca caa gta tct ggg cag att aag cat att tta 96
Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu
20 25 30

gta caa gaa gga cag aag gtt aaa aaa ggt gag cta tta gct gta att 144
Val Gln Glu Gly Gln Lys Val Lys Gly Glu Leu Leu Ala Val Ile
35 40 45

gat cca cgt ctg gct gaa acg gaa tta aaa cta gca aaa gct gag cta 192
Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu
50 55 60

gca aat gct tct gct aat ttg gat aca aaa aaa att aat ctt aag caa 240
Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln
65 70 75 80

ctg caa tca gat tgg gaa cgt cat caa cgt ttg ata cga acc aat gcg 288
Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala
85 90 95

aca agc caa aag gaa aca gaa gca aaa agt aga tta aat acg gcc 336
Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala
100 105 110

aaa gca gaa ctt caa att gcg caa aat aat cta gat atc gct aaa atc 384
Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile
115 120 125

aga gtg gaa aaa gct gaa acc gaa cta gga tat aca gaa att cgt tct 432
Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser
130 135 140

cca ctt gat gca aca gta att tca gta ttt gcg caa aat ggt caa act 480
Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr
145 150 155 160

tta gtc acc acc caa caa gta cca gtg ctg atg aaa tta gct aat at 527
Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn
165 170 175

<210> 131

<211> 175

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 131

Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu
1 5 10 15

Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu
20 25 30

Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile
35 40 45

Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu
50 55 60

Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln
65 70 75 80

Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala
85 90 95

Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala
100 105 110

Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile
115 120 125

Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser
130 135 140

Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr
145 150 155 160

Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn
165 170 175

<210> 132

<211> 867

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> atpG

<220>

<221> CDS

<222> (1)...(864)

<400> 132

atg gca ggt gcg aaa gag ata aga acc aaa att gca agt gtg aaa aat 48
Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn
1 5 10 15

act caa aaa atc acc aaa gca atg gaa atg gtt gct acc tct aaa atg 96
Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met
20 25 30

cgt aaa acg caa gag cgt atg gct gcc agt cgt cct tat tcg gaa aca 144
Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr
35 40 45

atc cgt aag gtg att agc cat att gcg aaa gga agc att ggt tat aag 192
Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys
50 55 60

cac ccg ttt tta act gaa cgt gat att aaa aaa gta ggc tat ctt gtc 240
His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val
65 70 75 80

gtt tcg acc gat cgc ggt tta tgc ggt ggc ctt aat atc aat tta ttc 288
Val Ser Thr Asp Arg Gly Leu Cys Gly Leu Asn Ile Asn Leu Phe
85 90 95

aaa gcg act ttg aat gaa ttt aaa acg tgg aaa gat aaa gac gtt agt 336
Lys Ala Thr Leu Asn Glu Phe Lys Thr Trp Lys Asp Lys Asp Val Ser
100 105 110

gtt gag ctt ggt tta gta ggg tcg aaa ggc gta agc ttt tac caa aat 384
Val Glu Leu Gly Leu Val Gly Ser Lys Gly Val Ser Phe Tyr Gln Asn
115 120 125

cta ggc tta aac gtg aga tct caa gta acg gga tta ggc gat aat ccg 432
Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro
130 135 140

gaa atg gaa cgt atc gtg ggc gca gtt aat gaa atg att aat gcg ttc 480
Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe
145 150 155 160

cga aac gga gaa gtg gat gcg gtt tac gtc gct tac aac cgt ttt gaa 528
Arg Asn Gly Glu Val Asp Ala Val Tyr Val Ala Tyr Asn Arg Phe Glu
165 170 175

aat acg atg tca caa aaa cct gtt atc gca cag tta ctt ccg tta cct 576
Asn Thr Met Ser Gln Lys Pro Val Ile Ala Gln Leu Leu Pro Leu Pro
180 185 190

aaa cta gat gac gat gaa tta gat acg aaa ggt tca tgg gat tat att 624
Lys Leu Asp Asp Asp Glu Leu Asp Thr Lys Gly Ser Trp Asp Tyr Ile
195 200 205

tat gaa ccg aat cca caa gtt tta ttg gat agt tta ctt gtt cgt tat 672
Tyr Glu Pro Asn Pro Gln Val Leu Leu Asp Ser Leu Leu Val Arg Tyr
210 215 220

tta gaa act cag gta tac caa gca gtt gta gat aac cta gct tct gaa	720
Leu Glu Thr Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu	
225 230 235 240	
caa gcc gct cga atg gta gcg atg aaa gcc gca aca gat aat gcg ggt	768
Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly	
245 250 255	
aca tta atc gat gaa tta caa tta gtg tat aac aaa gct cgc caa gca	816
Thr Leu Ile Asp Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala	
260 265 270	
agc att aca aat gaa tta aac gaa att gtt gcg ggt gcc gca gca att	864
Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile	
275 280 285	
taa	867

<210> 133
<211> 288
<212> PRT
<213> *Actinobacillus pleuropneumoniae*

<400> 133
Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn
1 5 10 15

Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met
20 25 30

Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr
35 40 45

Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys
50 55 60

His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val
65 70 75 80

Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe
85 90 95

Lys Ala Thr Leu Asn Glu Phe Lys Thr Trp Lys Asp Lys Asp Val Ser
100 105 110

Val Glu Leu Gly Leu Val Gly Ser Lys Gly Val Ser Phe Tyr Gln Asn
115 120 125

Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro
130 135 140

Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe
145 150 155 160

Arg Asn Gly Glu Val Asp Ala Val Tyr Val Ala Tyr Asn Arg Phe Glu
165 170 175

Asn Thr Met Ser Gln Lys Pro Val Ile Ala Gln Leu Leu Pro Leu Pro
180 185 190

Lys Leu Asp Asp Asp Glu Leu Asp Thr Lys Gly Ser Trp Asp Tyr Ile
195 200 205

Tyr Glu Pro Asn Pro Gln Val Leu Leu Asp Ser Leu Leu Val Arg Tyr
210 215 220

Leu Glu Thr Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu
225 230 235 240

Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly
245 250 255

Thr Leu Ile Asp Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala
260 265 270

Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile
275 280 285

<210> 134

<211> 534

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> atpH

<220>

<221> CDS

<222> (1)..(531)

<400> 134

atg tca gaa tta agt aca gta gct cgc ccc tac gct aaa gca gct ttt 48
Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
1 5 10 15

gat ttt gct tta gaa caa ggt cag ttg gac aaa tgg caa gaa atg tta 96
Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu
20 25 30

cag ttt tcg gca ttc gtt gct gaa aac gaa caa gtg gcg gaa tat att 144
Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile
35 40 45

aat tct tcc ctt gca agc ggt cag att tct gaa act ttt atc aaa atc 192
Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile
50 55 60

tgc ggc gac caa ctt gat caa tat ggg caa aat ttt att cgt gta atg 240
Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met
65 70 75 80

gct gaa aat aaa cgt ctg gct gtg ttg cct atg gtt ttt gat act ttc 288
Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe
85 90 95

gta tca tta cga gcg gaa cat gaa gcg gta aaa gat gta aca att gtt 336
Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val
100 105 110

tcg gca aac gaa tta agt caa gca caa gaa gat aaa atc gca aaa gcg 384
Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala
115 120 125

atg gaa aaa cgc tta ggt caa aaa gtt cgt tta acc aac caa atc gat 432
Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp

130

135

140

aac agc ctg att gca ggc gta att att aaa tac gat gat gtt gtt att 480
Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile
145 150 155 160

gat ggt agt agc cgc ggt cag tta aat cgc tta gcg tca gcg ttg agc 528
Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser
165 170 175

ttg taa 534
Leu

<210> 135
<211> 177
<212> PRT
<213> *Actinobacillus pleuropneumoniae*

<400> 135
Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
1 5 10 15

Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu
20 25 30

Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile
35 40 45

Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile
50 55 60

Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met
65 70 75 80

Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe
85 90 95

Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val
100 105 110

Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala
115 120 125

Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp
130 135 140

Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile
145 150 155 160

Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser
165 170 175

Leu

<210> 136
<211> 321
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>

<223> dksA

<220>

<221> CDS

<222> (1) .. (318)

<400> 136

gca tgg cat gtg caa att atg gac gaa gct gag cgt aca aaa aac caa 4
Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
1 5 10 15

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atg cag gaa gaa gtc gct aat ttc gcc gat cct gcg gac cgc gcc act 96
Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
20          25          30

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cag gaa gaa gaa ttc agt ctt gaa tta aga aac cgt gac cgt gag cgt 144
 Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg
 35 40 45

aaa ttg ctt aag aag att gag caa acg tta aat agc att gcc gaa gac 192
 Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp
 50 55 60

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gaa tac ggc tat tgc gaa act tgc ggt gtt gaa atc ggt tta cgt cgt 240
Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg
   65           70           75           80

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tta gaa gcg cgc ccg acc gcg gat atg tgt atc gat tgc aaa aca ctt	288
Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu	
85 90 95	

gcg gaa atc cgt gaa aag caa atg ggc tta taa 321
Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
100 105

<210> 137

<211> 106

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 137

Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
1 5 10 15

Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
20 25 30

Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Arg Asp Arg Glu Arg
 35 40 45

Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp
 50 55 60

Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg
65 70 75 80

Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu
85 90 95

Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
100 105

<210> 138
<211> 33
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> *dnaK*

<220>
<221> CDS
<222> (1)..(30)

<400> 138
gct gag ttt gaa gaa gtg aaa gat aat aaa taa 33
Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
1 5 10

<210> 139
<211> 10
<212> PRT
<213> *Actinobacillus pleuropneumoniae*

<400> 139
Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
1 5 10

<210> 140
<211> 453
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> *exbB*

<220>
<221> CDS
<222> (1)..(450)

<400> 140
atg gaa caa atg ctt gaa ctt tta caa ggt cat gtt gat tat att att 48
Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile
1 5 10 15

tta ggc tta tta cta tta atg agt gtt gtg ttg gta tgg aaa att att 96
Leu Gly Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile
20 25 30

gaa cgc gta ctt ttc tac aaa caa ttg gat gtg acc aaa tat gac acg 144
Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr
35 40 45

cta caa gat ttg gaa att gat acc act cgc aat tta acc acc att tcc 192
Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser
50 55 60

act atc ggt gcc aac gcc cct tat atc ggt tta tta gga acc gta tta 240
Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu
65 70 75 80

ggg atc tta ctt acc ttc tat cat tta ggg cat tcc ggc ggt gat att 288
Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile

	85	90	95	
gac gcc gca tcc att atg gtt cac ctt tcg ctt gca tta aaa gca acc				336
Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr				
100	105		110	
gca gcc ggt atc tta gtc gct att ccg gca atg atg ttc tac agc ggt				384
Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly				
115	120		125	
ttt aac cgt aaa gtg gat gaa agc aaa ctt aaa tgg caa gcg att caa				432
Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln				
130	135		140	
gct cgt aaa gcc aat caa taa				453
Ala Arg Lys Ala Asn Gln				
145	150			
<210> 141				
<211> 150				
<212> PRT				
<213> <i>Actinobacillus pleuropneumoniae</i>				
<400> 141				
Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile				
1	5	10	15	
Leu Gly Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile				
20	25		30	
Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr				
35	40		45	
Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser				
50	55		60	
Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu				
65	70		75	80
Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile				
85	90		95	
Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr				
100	105		110	
Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly				
115	120		125	
Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln				
130	135		140	
Ala Arg Lys Ala Asn Gln				
145	150			
<210> 142				
<211> 720				
<212> DNA				
<213> <i>Actinobacillus pleuropneumoniae</i>				
<220>				
<223> fkpA				

<220>
<221> CDS
<222> (1)..(717)

<400> 142
atg tta aaa aat aaa ctt tct gtt ctt gca atc gta gcc ggt acg ttc 48
Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe
1 5 10 15

gtt tca gct caa act gca ttt gca gcg gat caa aaa ttc att gac gat 96
Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp
20 25 30

tca tca tat gca gtc ggc gta ttg atg ggt aaa aat atc gaa ggc gtc 144
Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val
35 40 45

gtt gaa tca caa aaa gaa att ttt tct tat aac caa gat aaa atc ttg 192
Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu
50 55 60

gcg ggt gtc caa gat acc atc aaa aaa acc ggt aaa tta acc gat gaa 240
Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu
65 70 75 80

gat cta caa aaa caa tta aaa tcg ctt gat act tat ctt gca agt caa 288
Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln
85 90 95

gaa agc aaa att gcg gcg gag aaa agc aaa gca acc gta gaa gcc ggt 336
Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly
100 105 110

aat aaa ttt cgt acc gac tac gaa aaa caa agc ggc gtg aaa aaa acc 384
Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr
115 120 125

gct tcc ggt tta ctt tat aaa att gaa aaa gcc ggc acg ggc gaa tcg 432
Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser
130 135 140

cct aaa gcg gaa gat acc gtt aaa gtt cac tat aaa ggg aca tta acc 480
Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr
145 150 155 160

gat ggt acg gta ttc gat agc tca tac gat cgc ggt gag ccg att gaa 528
Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu
165 170 175

ttc caa tta aac caa tta att ccg ggt tgg att gaa gcg att cca atg 576
Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met
180 185 190

ttg aaa aaa ggc gga aaa atg gaa atc gtc gtt ccg cct gaa ctt ggt 624
Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly
195 200 205

tac ggc gaa cgc caa gca ggt aag att ccg gca agt tca acc tta aaa 672
Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys
210 215 220

ttc gag att gaa ttg tta gat ttc aaa gcg gcc gaa gcg aaa aaa taa 720
Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys

225

230

235

<210> 143

<211> 239

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 143

Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe
1 5 10 15

Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp
20 25 30

Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val
35 40 45

Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu
50 55 60

Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu
65 70 75 80

Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln
85 90 95

Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly
100 105 110

Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr
115 120 125

Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser
130 135 140

Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr
145 150 155 160

Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu
165 170 175

Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met
180 185 190

Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly
195 200 205

Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys
210 215 220

Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys
225 230 235

<210> 144

<211> 290

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> HI0379

<220>
<221> CDS
<222> (3)...(287)

<400> 144
tg cat agc gtg aga ggt ccg ggc ggc ggt tat caa ctc ggt aag caa 47
His Ser Val Arg Gly Pro Gly Gly Tyr Gln Leu Gly Lys Gln
1 5 10 15

cct gaa gag att agt gtg ggg atg att att gcg gcg gtg aat gaa aat 95
Pro Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn
20 25 30

ctc gac gta acc aaa tgt aaa ggt agc ggc aac tgt agc aaa aac tct 143
Leu Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser
35 40 45

cag tgc tta acc cat cat tta tgg gaa cgt tta gaa gaa caa atc ggt 191
Gln Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly
50 55 60

gtg ttt tta aat acg att act tta gcg gaa ctt gtt gaa gaa cat tcg 239
Val Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser
65 70 75

gat cac gat tgt gaa aaa gaa cat tgc cac gat cat tca cac aaa cat 287
Asp His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His
80 85 90 95

taa 290

<210> 145
<211> 95
<212> PRT
<213> *Actinobacillus pleuropneumoniae*

<400> 145
His Ser Val Arg Gly Pro Gly Gly Tyr Gln Leu Gly Lys Gln Pro 15
1 5 10 15

Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn Leu
20 25 30

Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser Gln
35 40 45

Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly Val
50 55 60

Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser Asp
65 70 75 80

His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His
85 90 95

<210> 146
<211> 273
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>

<223> hupA

<220>

<221> CDS

<222> (1)..(270)

<400> 146

atg aac aaa act gag tta atc gat gca atc gca gct ggt gca gag tta	48
Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu	
1 5 10 15	

agc aag aaa gac gcg aaa gcg gca tta gaa gcg act tta aat gcg atc	96
Ser Lys Lys Asp Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile	
20 25 30	

tct gaa agc cta aaa aat ggc gac acc gtt cag tta atc ggc ttc ggt	144
Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly	
35 40 45	

act ttt aaa gta aac gag cgt aat gca cgt acg ggt cgt aac ccg cgt	192
Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg	
50 55 60	

acc ggc gaa gaa atc aaa atc gca gca tct aaa gtg ccg gcg ttt gtt	240
Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val	
65 70 75 80	

gca ggt aaa gca tta aaa gat tta gta aaa taa	273
Ala Gly Lys Ala Leu Lys Asp Leu Val Lys	
85 90	

<210> 147

<211> 90

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 147

Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu	
1 5 10 15	

Ser Lys Lys Asp Ala Lys Ala Leu Glu Ala Thr Leu Asn Ala Ile	
20 25 30	

Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly	
35 40 45	

Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg	
50 55 60	

Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val	
65 70 75 80	

Ala Gly Lys Ala Leu Lys Asp Leu Val Lys	
85 90	

<210> 148

<211> 551

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> 1pdA

<220>

<221> CDS

<222> (1) .. (549)

<400> 148

atg agc aaa gaa atc aaa acg caa gtc gtg gta ctt ggt gcg ggt cct 48
Met Ser Lys Glu Ile Lys Thr Gln Val Val Val Leu Gly Ala Gly Pro
1 5 10 15

gcc ggt tat tca gcg gca ttc cgt tgt gcc gac tta ggc tta gaa aca 96
Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr
20 25 30

gta att gtc gaa cgt tat tca act ttg ggc ggt gta tgc tta aac gta 144
Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val
35 40 45

ggt tgt att ccg tct aaa gca tta tta cac gtt gca aaa gtt atc gaa 192
Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu
50 55 60

gaa gca aaa cac gca gag aaa aac ggt att act ttc ggt gag ccc aac 240
Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn
65 70 75 80

att gat tta gat aaa gtg cgt gcg ggt aaa gaa gcg gtt gtt tct aaa 288
Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys
85 90 95

tta acc ggc ggt tta gcg ggt atg gct aaa gca cgt aaa gta aca gta 336
Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val
100 105 110

gtg gaa ggt tta gcg gcg ttt acc gat ccg aat act tta gta gct cgt 384
Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg
115 120 125

gac cgt gac ggt aat ccg aca acg att aaa ttt gat tat gca att att 432
Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile
130 135 140

gca gcc ggt tct cgt ccg att cag ctt ccg ttc att cca cac gaa gat 480
Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp
145 150 155 160

ccg cgt gtg tgg gat tct acg gat gca ctt aaa tta aaa gaa gta ccc 528
Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro
165 170 175

gaa aaa att act cat tat ggg cc 551
Glu Lys Ile Thr His Tyr Gly
180

<210> 149

<211> 183

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 149

Met Ser Lys Glu Ile Lys Thr Gln Val Val Val Leu Gly Ala Gly Pro

1	5	10	15												
Ala	Gly	Tyr	Ser	Ala	Ala	Phe	Arg	Cys	Ala	Asp	Leu	Gly	Leu	Glu	Thr
				20				25					30		
Val	Ile	Val	Glu	Arg	Tyr	Ser	Thr	Leu	Gly	Gly	Val	Cys	Leu	Asn	Val
			35				40					45			
Gly	Cys	Ile	Pro	Ser	Lys	Ala	Leu	Leu	His	Val	Ala	Lys	Val	Ile	Glu
					50		55					60			
Glu	Ala	Lys	His	Ala	Glu	Lys	Asn	Gly	Ile	Thr	Phe	Gly	Glu	Pro	Asn
	65				70				75				80		
Ile	Asp	Leu	Asp	Lys	Val	Arg	Ala	Gly	Lys	Glu	Ala	Val	Val	Ser	Lys
			85					90				95			
Leu	Thr	Gly	Gly	Leu	Ala	Gly	Met	Ala	Lys	Ala	Arg	Lys	Val	Thr	Val
				100				105				110			
Val	Glu	Gly	Leu	Ala	Ala	Phe	Thr	Asp	Pro	Asn	Thr	Leu	Val	Ala	Arg
				115			120				125				
Asp	Arg	Asp	Gly	Asn	Pro	Thr	Thr	Ile	Lys	Phe	Asp	Tyr	Ala	Ile	Ile
				130			135				140				
Ala	Ala	Gly	Ser	Arg	Pro	Ile	Gln	Leu	Pro	Phe	Ile	Pro	His	Glu	Asp
	145				150				155				160		
Pro	Arg	Val	Trp	Asp	Ser	Thr	Asp	Ala	Leu	Lys	Leu	Lys	Glu	Val	Pro
			165					170				175			
Glu	Lys	Ile	Thr	His	Tyr	Gly									
			180												
<210>	150														
<211>	1095														
<212>	DNA														
<213>	Actinobacillus pleuropneumoniae														
<220>															
<223>	Omp5-2														
<220>															
<221>	CDS														
<222>	(1)..(1092)														
<400>	150														
atg	aaa	aaa	tca	tta	gtt	gct	tta	aca	gtt	tta	tcg	gct	gca	gcg	gtt
Met	Lys	Lys	Ser	Leu	Val	Ala	Leu	Thr	Val	Leu	Ser	Ala	Ala	Ala	Val
1				5					10				15		
gct	caa	gca	gcg	cca	caa	aat	act	ttc	tac	gca	ggt	gcg	aaa	gca	
Ala	Gln	Ala	Ala	Pro	Gln	Gln	Asn	Thr	Phe	Tyr	Ala	Gly	Ala	Lys	Ala
				20				25				30			96
ggt	tgg	gct	tca	ttc	cat	gat	ggt	atc	gaa	caa	tta	gat	tca	gct	aaa
Gly	Trp	Ala	Ser	Phe	His	Asp	Gly	Ile	Glu	Gln	Leu	Asp	Ser	Ala	Lys
				35			40					45			144
aac	aca	gat	cgc	ggt	aca	aaa	tac	ggt	atc	aac	cgt	aat	tca	gta	act
Asn	Thr	Asp	Arg	Gly	Thr	Lys	Tyr	Gly	Ile	Asn	Arg	Asn	Ser	Val	Thr
													192		

50	55	60	
tac ggc gta ttc ggc ggt tac caa att tta aac caa gac aaa tta ggt Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly	65	70	240
		75	80
tta gcg gct gaa tta ggt tat gac tat ttc ggt cgt gtg cgc ggt tct Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser		85	288
		90	95
gaa aaa cca aac ggt aaa gcg gac aag aaa act ttc cgt cac gct gca Glu Lys Pro Asn Gly Lys Ala Asp Lys Lys Thr Phe Arg His Ala Ala		100	336
		105	110
cac ggt gcg aca atc gca tta aaa cct agc tac gaa gta tta cct gac His Gly Ala Thr Ile Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp		115	384
		120	125
tta gac gtt tac ggt aaa gta ggt atc gca tta gta aac aat aca tat Leu Asp Val Tyr Gly Lys Val Gly Ile Ala Leu Val Asn Asn Thr Tyr		130	432
		135	140
aaa aca ttc aat gca gca caa gag aaa gtg aaa act cgt cgt ttc caa Lys Thr Phe Asn Ala Ala Gln Glu Lys Val Lys Thr Arg Arg Phe Gln		145	480
		150	155
agt tct tta att tta ggt gcg ggt gtt gag tac gca att ctt cct gaa Ser Ser Leu Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro Glu		165	528
		170	175
tta gcg gca cgt gtt gaa tac caa tgg tta aac aac gca ggt aaa gca Leu Ala Ala Arg Val Glu Tyr Gln Trp Leu Asn Asn Ala Gly Lys Ala		180	576
		185	190
agc tac tct act tta aat cgt atg ggt gca act gac tac cgt tcg gat Ser Tyr Ser Thr Leu Asn Arg Met Gly Ala Thr Asp Tyr Arg Ser Asp		195	624
		200	205
atc agt tcc gta tct gca ggt tta agc tac cgt ttc ggt caa ggt gcg Ile Ser Ser Val Ser Ala Gly Leu Ser Tyr Arg Phe Gly Gln Gly Ala		210	672
		215	220
gca ccg gtt gca gct ccg gca gtt gaa act aaa aac ttc gca ttc agc Ala Pro Val Ala Ala Pro Ala Val Glu Thr Lys Asn Phe Ala Phe Ser		225	720
		230	235
240			
tct gac gta tta ttc gca ttc ggt aaa tca aac tta aaa ccg gct gcg Ser Asp Val Leu Phe Ala Phe Gly Lys Ser Asn Leu Lys Pro Ala Ala		245	768
		250	255
gca aca gca tta gat gca atg caa acc gaa atc aat aac gca ggt tta Ala Thr Ala Leu Asp Ala Met Gln Thr Glu Ile Asn Asn Ala Gly Leu		260	816
		265	270
tca aat gct gcg atc caa gta aac ggt tac acg gac cgt atc ggt aaa Ser Asn Ala Ala Ile Gln Val Asn Gly Tyr Thr Asp Arg Ile Gly Lys		275	864
		280	285
gaa gct tca aac tta aaa ctt tca caa cgt cgt gcg gaa aca gta gct Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg Ala Glu Thr Val Ala		290	912
		295	300
aac tac atc gtt tct aaa ggt gct ccg gca gct aac gta act gca gta			960

Asn Tyr Ile Val Ser Lys Gly Ala Pro Ala Ala Asn Val Thr Ala Val
305 310 315 320
ggt tac ggt gaa gca aac cct gta acc ggc gca aca tgt gac aaa gtt 1008
Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala Thr Cys Asp Lys Val
325 330 335
aaa ggt cgt aaa gca tta atc gct tgc tta gca ccg gat cgt cgt gtt 1056
Lys Gly Arg Lys Ala Leu Ala Cys Leu Ala Pro Asp Arg Arg Val
340 345 350
gaa gtt caa gtt caa ggt act aaa gaa gta act atg taa 1095
Glu Val Gln Val Gln Gly Thr Lys Glu Val Thr Met
355 360

<210> 151
<211> 364
<212> PRT
<213> *Actinobacillus pleuropneumoniae*

<400> 151
Met Lys Lys Ser Leu Val Ala Leu Thr Val Leu Ser Ala Ala Ala Val
1 5 10 15
Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Ala
20 25 30
Gly Trp Ala Ser Phe His Asp Gly Ile Glu Gln Leu Asp Ser Ala Lys
35 40 45
Asn Thr Asp Arg Gly Thr Lys Tyr Gly Ile Asn Arg Asn Ser Val Thr
50 55 60
Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly
65 70 75 80
Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser
85 90 95
Glu Lys Pro Asn Gly Lys Ala Asp Lys Lys Thr Phe Arg His Ala Ala
100 105 110
His Gly Ala Thr Ile Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp
115 120 125
Leu Asp Val Tyr Gly Lys Val Gly Ile Ala Leu Val Asn Asn Thr Tyr
130 135 140
Lys Thr Phe Asn Ala Ala Gln Glu Lys Val Lys Thr Arg Arg Phe Gln
145 150 155 160
Ser Ser Leu Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro Glu
165 170 175
Leu Ala Ala Arg Val Glu Tyr Gln Trp Leu Asn Asn Ala Gly Lys Ala
180 185 190
Ser Tyr Ser Thr Leu Asn Arg Met Gly Ala Thr Asp Tyr Arg Ser Asp
195 200 205
Ile Ser Ser Val Ser Ala Gly Leu Ser Tyr Arg Phe Gly Gln Gly Ala
210 215 220

Ala Pro Val Ala Ala Pro Ala Val Glu Thr Lys Asn Phe Ala Phe Ser
225 230 235 240
Ser Asp Val Leu Phe Ala Phe Gly Lys Ser Asn Leu Lys Pro Ala Ala
245 250 255
Ala Thr Ala Leu Asp Ala Met Gln Thr Glu Ile Asn Asn Ala Gly Leu
260 265 270
Ser Asn Ala Ala Ile Gln Val Asn Gly Tyr Thr Asp Arg Ile Gly Lys
275 280 285
Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg Ala Glu Thr Val Ala
290 295 300
Asn Tyr Ile Val Ser Lys Gly Ala Pro Ala Ala Asn Val Thr Ala Val
305 310 315 320
Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala Thr Cys Asp Lys Val
325 330 335
Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala Pro Asp Arg Arg Val
340 345 350
Glu Val Gln Val Gln Gly Thr Lys Glu Val Thr Met
355 360

<210> 152
<211> 1110
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> Omp5

<220>
<221> CDS
<222> (1)..(1107)

<400> 152
atg aaa aaa tca tta gtt gct tta gca gta tta tcg gct gca gca gta 48
Met Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Ala Val
1 5 10 15
gct caa gca gct cca caa aat act ttc tac gca ggt gcg aaa gtt 96
Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val
20 25 30
ggc caa tca tca ttt cac cac ggt gtt aac caa tta aaa tct ggt cac 144
Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His
35 40 45
gat gat cgt tat aat gat aaa aca cgt aag tat ggt atc aac cgt aac 192
Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn
50 55 60
tct gta act tac ggt gta ttc ggc ggt tac caa atc tta aac caa aat 240
Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn
65 70 75 80
aac ttc ggt tta gca gct gaa tta ggc tat gac tac tac ggt cgc gta 288
Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Tyr Gly Arg Val

85	90	95	
cgt ggt aac gta gat gaa ttc cgt aca gtt aaa cac tct gct cac ggt Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly 100	105	110	336
tta aac tta gcg tta aaa cca agc tac gaa gta tta cct gac tta gac Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp 115	120	125	384
gtt tac ggt aaa gta ggt att gcg gtt cgt aat gac tat aaa aaa Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys 130	135	140	432
tat ggt gcg gaa aac act aac gaa tca aca aca aaa ttc cac aaa tta Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu 145	150	155	480
aaa gca tca act att tta ggt gca ggt gtt gag tac gca att ctt cct Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro 165	170	175	528
gaa tta gcg gca cgt gtt gaa tac caa tac tta aac aaa gcg ggt aac Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn 180	185	190	576
tta aat aaa gca tta gtt cgt tca ggc aca caa gat gtg gac ttc caa Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln 195	200	205	624
tat gct cct gat atc cac tct gta aca gca ggt tta tca tac cgt ttc Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe 210	215	220	672
ggc caa ggc gct gta gca cca gtt gtt gag cca gaa gtt gta act aaa Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys 225	230	235	720
aac ttc gca ttc agc tca gac gtt tta ttt gat ttc ggt aaa tca agc Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser 245	250	255	768
tta aaa cca gca gca aca gct tta gac gca gct aac act gaa atc Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile 260	265	270	816
gct aac tta ggt tta gca act cca gct atc caa gtt aac ggt tat aca Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr 275	280	285	864
gac cgt atc ggt aaa gaa gct tca aac tta aaa ctt tca caa cgc cgt Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg 290	295	300	912
gca gaa act gta gct aac tac tta gtt tct aaa ggt caa aac cct gca Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala 305	310	315	960
aac gta act gca gta ggt tac ggt gaa gca aac cca gta acc ggc gca Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala 325	330	335	1008
aca tgt gat gca gtt aaa ggt cgt aaa gca tta atc gct tgc tta gca			1056

Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala
340 345 350

ccg gat cgt cgt gtt gaa gtt caa gta caa ggt gct aaa aac gta gct 1104
Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala
355 360 365

atg taa 1110
Met

<210> 153
<211> 369
<212> PRT
<213> *Actinobacillus pleuropneumoniae*

<400> 153
Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Ala Val
1 5 10 15

Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val
20 25 30

Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His
35 40 45

Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn
50 55 60

Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn
65 70 75 80

Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Tyr Gly Arg Val
85 90 95

Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly
100 105 110

Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp
115 120 125

Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys
130 135 140

Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu
145 150 155 160

Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro
165 170 175

Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn
180 185 190

Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln
195 200 205

Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe
210 215 220

Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys
225 230 235 240

Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser

245	250	255
Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile		
260	265	270
Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr		
275	280	285
Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg		
290	295	300
Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala		
305	310	315
Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala		
325	330	335
Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala		
340	345	350
Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala		
355	360	365

Met

<210> 154
<211> 1076
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> pnp new

<220>
<221> CDS
<222> (1)..(1074)

<400> 154

aat att aaa gaa ttc gta aaa gaa gcg ggt aaa ccg cgt tgg gat tgg	48
Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp	
1 5 10 15	

gtt gcg ccg gaa ccg aat acc gca tta atc aac caa gtt aaa gcg tta 96

Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu	
20 25 30	

gct gaa gct cgt atc ggc gat gct tat cgt att aca gaa aaa caa gct 144

Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala	
35 40 45	

cgt tac gaa caa atc gat gca att aaa gct gat gtt atc gca caa tta 192

Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu	
50 55 60	

acc gca caa gac gaa acc gtt tct gaa ggt gct att att gat att att 240

Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile	
65 70 75 80	

acc gca tta gaa agt tct att gtt cgc ggt cgt att att gcc ggc gaa 288

Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu	
85 90 95	

ccg cgt att gac ggt cgt acg gta gat acg gtt cgt gca tta gac att	336
Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile	
100 105 110	
tgc acc ggc gta tta cct cgt acg cac ggt tct gca atc ttt act cgc	384
Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg	
115 120 125	
ggt gaa aca caa gca tta gcg gtt gca acc tta ggt act gag cgc gat	432
Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp	
130 135 140	
gca caa att gtt gac gaa tta acc ggc gag aaa tca gac cgt ttc tta	480
Ala Gln Ile Val Asp Glu Leu Thr Gly Glu Lys Ser Asp Arg Phe Leu	
145 150 155 160	
ttc cac tat aac ttc cct ccg tac tct gtc ggt gaa acc ggt cgt atc	528
Phe His Tyr Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Arg Ile	
165 170 175	
ggt tcg ccg aaa cgt cgt gaa atc ggc cac ggt cgt tta gcg aaa cgc	576
Gly Ser Pro Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg	
180 185 190	
ggt gta tta gcg gta atg ccg act gct gaa gaa ttc ccg tat gta gtg	624
Gly Val Ileu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val	
195 200 205	
cgc gta gta tct gaa att acc gaa tca aac ggt tct tct tca atg gct	672
Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala	
210 215 220	
tcc gta tgc ggc gca tct tta gcg tta atg gac gca ggc gta ccg att	720
Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile	
225 230 235 240	
aaa gcg gcg gtt gcg ggt atc gca atg ggc tta gtg aaa gaa gaa gaa	768
Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu	
245 250 255	
aaa ttt gtg gtg ctt tca gac atc tta ggt gac gaa gac cat tta ggc	816
Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly	
260 265 270	
gat atg gac ttc aaa gta gcc ggt acg cgt gaa ggt gta acc gca ctt	864
Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu	
275 280 285	
caa atg gat att aaa atc gaa ggt atc acg cct gaa att atg caa atc	912
Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile	
290 295 300	
gca tta aat caa gcg aaa ggt gcg cgt atg cac atc tta agc gtg atg	960
Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met	
305 310 315 320	
gaa caa gcg att cct gca cct cgt gcc gat att tcc gat ttt gcg cct	1008
Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro	
325 330 335	
cgt att cat acg atg aag atc gat ccg aag aaa atc aaa gac gtg atc	1056
Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile	
340 345 350	

ggt aaa ggc ggt gcg gtt at 1076
Gly Lys Gly Gly Ala Val
355

<210> 155
<211> 358
<212> PRT
<213> **Actinobacillus pleuropneumoniae**

<400> 155
Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp
1 5 10 15

Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu
20 25 30

Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala
35 40 45

Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu
50 55 60

Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile
65 70 75 80

Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu
85 90 95

Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile
100 105 110

Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg
115 120 125

Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp
130 135 140

Ala Gln Ile Val Asp Glu Leu Thr Gly Glu Lys Ser Asp Arg Phe Leu
145 150 155 160

Phe His Tyr Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Arg Ile
165 170 175

Gly Ser Pro Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg
180 185 190

Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val
195 200 205

Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala
210 215 220

Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile
225 230 235 240

Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu
245 250 255

Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly
260 265 270

Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu

	275	280	285	
Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile				
290	295		300	
Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met				
305	310	315		320
Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro				
325	330		335	
Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile				
340	345		350	
Gly Lys Gly Gly Ala Val				
355				
<210> 156				
<211> 1055				
<212> DNA				
<213> <i>Actinobacillus pleuropneumoniae</i>				
<220>				
<223> potD				
<220>				
<221> CDS				
<222> (1)..(1053)				
<400> 156				
atg aaa aaa tta gcg ggt tta ttt gca gca ggt tta gcg aca gtt gca				48
Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala				
1	5	10		15
tta aca gcg tgg aat gaa gaa aag cca aaa gcg gct gaa gca gcg gct				96
Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala				
20	25		30	
caa ccg gca gca gcg gga aca gtt cac ctt tat act tgg act gaa tat				144
Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr				
35	40		45	
gtg cct gaa ggc ttg tta gat gaa ttt aca aag caa acc acc ggt atc aaa				192
Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys				
50	55	60		
gta gag gtt tca agc ctt gaa tct aac gaa acc atg tat gcg aaa tta				240
Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu				
65	70	75	80	
aaa tta caa ggt aaa gac ggc ggt tac gat gtt atc gca cct tct aac				288
Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn				
85	90		95	
tac ttc gtt tca aaa atg gcg aaa gaa ggt atg tta gcg gaa tta gat				336
Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp				
100	105		110	
cac gca aaa ctt cct gta atc aaa gag tta aac caa gat tgg tta aac				384
His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn				
115	120		125	

aaa cct tat gac caa ggt aac aaa tac tct tta ccg caa tta tta ggt	432
Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly	
130 135 140	
gca ccg ggt atc gca ttt aac tca aat gac tat aag ggc gat gcg ttc	480
Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe	
145 150 155 160	
act tct tgg ggt gat tta tgg aaa cct gag ttt gcg aat aaa gta caa	528
Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln	
165 170 175	
tta tta gat gac gca cgt gaa gta ttt aac att gcg tta tta aaa tta	576
Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu	
180 185 190	
ggt aaa aac cct aat aca acc aat ccg gaa gag att aaa gcg gct tac	624
Gly Lys Asn Pro Asn Thr Thr Asn Pro Glu Glu Ile Lys Ala Ala Tyr	
195 200 205	
gaa gag tta aga aaa tta cgt cca aac gta ctt tct ttc act tca gac	672
Glu Glu Leu Arg Lys Leu Arg Pro Asn Val Leu Ser Phe Thr Ser Asp	
210 215 220	
aac cca gcg aac tca ttt atc gca ggt gaa gta tct gta ggt caa tta	720
Asn Pro Ala Asn Ser Phe Ile Ala Gly Glu Val Ser Val Gly Gln Leu	
225 230 235 240	
tgg aac ggt tct gta cgt att gcg aaa aaa gaa caa gca gcg ccg gta aac	768
Trp Asn Gly Ser Val Arg Ile Ala Lys Lys Glu Gln Ala Pro Val Asn	
245 250 255	
atg gtg ttc cca aaa gaa ggt cct gta ctt tgg gtt gat acg tta gcc	816
Met Val Phe Pro Lys Glu Gly Pro Val Leu Trp Val Asp Thr Leu Ala	
260 265 270	
att ccg gcg aat gcg aaa aac aaa gaa aat gcg cat aag tta atc aac	864
Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn	
275 280 285	
tac tta tta agc gca ccg gtt gcg gaa aaa tta acg tta gaa atc ggt	912
Tyr Leu Leu Ser Ala Pro Val Ala Glu Lys Leu Thr Leu Glu Ile Gly	
290 295 300	
tat ccg act tca aac gta gaa gcg tta aaa aca tta cca aaa gag att	960
Tyr Pro Thr Ser Asn Val Glu Ala Leu Lys Thr Leu Pro Lys Glu Ile	
305 310 315 320	
acc gaa gat ccg gca atc tat ccg aca gct gat gtg tta aaa gcg gca	1008
Thr Glu Asp Pro Ala Ile Tyr Pro Thr Ala Asp Val Leu Lys Ala Ala	
325 330 335	
caa tgg caa gac gat gta ggt aat gca atc gaa ctt tac gaa aaa ta	1055
Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys	
340 345 350	

<210> 157

<211> 351

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 157

Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala
1 5 10 15

Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala
20 25 30

Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr
35 40 45

Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys
50 55 60

Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu
65 70 75 80

Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn
85 90 95

Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp
100 105 110

His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn
115 120 125

Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly
130 135 140

Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe
145 150 155 160

Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln
165 170 175

Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu
180 185 190

Gly Lys Asn Pro Asn Thr Thr Asn Pro Glu Glu Ile Lys Ala Ala Tyr
195 200 205

Glu Glu Leu Arg Lys Leu Arg Pro Asn Val Leu Ser Phe Thr Ser Asp
210 215 220

Asn Pro Ala Asn Ser Phe Ile Ala Gly Glu Val Ser Val Gly Gln Leu
225 230 235 240

Trp Asn Gly Ser Val Arg Ile Ala Lys Lys Glu Gln Ala Pro Val Asn
245 250 255

Met Val Phe Pro Lys Glu Gly Pro Val Leu Trp Val Asp Thr Leu Ala
260 265 270

Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn
275 280 285

Tyr Leu Leu Ser Ala Pro Val Ala Glu Lys Leu Thr Leu Glu Ile Gly
290 295 300

Tyr Pro Thr Ser Asn Val Glu Ala Leu Lys Thr Leu Pro Lys Glu Ile
305 310 315 320

Thr Glu Asp Pro Ala Ile Tyr Pro Thr Ala Asp Val Leu Lys Ala Ala
325 330 335

Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys
340 345 350

<210> 158
<211> 525
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> rpmF

<220>
<221> CDS
<222> (1)...(522)

<400> 158
atg caa aag gta aaa cta ccc ctc acc att gac cca tat aaa gac gct 48
Met Gln Lys Val Lys Leu Pro Leu Thr Ile Asp Pro Tyr Lys Asp Ala
1 5 10 15
cag cgt cga atg gat tac gaa ggc tac atc tca cgt agt ctg ctt aat 96
Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn
20 25 30
cgt ttg ggt gaa tct gtg agc aat gtg cta agc gat gca caa gtt act 144
Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr
35 40 45
ctc tcg tta tat atc gat ccg caa cgc tta acc gtt att aaa ggt acg 192
Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr
50 55 60
gcg aca gtg gaa gtg gaa ttc gat tgc caa cga tgc ggt aac ccg ttt 240
Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe
65 70 75 80
aca caa acg ctt gac tgg tgg ttt tgg agt ccg gtt tcc aat atg 288
Thr Gln Thr Leu Asp Cys Ser Phe Cys Ser Pro Val Ser Asn Met
85 90 95
gat cag gcg gac aat ttg ccc gaa att tat gaa cca atc gaa gta aac 336
Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn
100 105 110
gag ttc ggt gaa gta aat tta cta gat atg atc gaa gat gga ttt atc 384
Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile
115 120 125
atc gaa ttg cct cta gtc ccg atg cat agt gaa gaa cac tgg gaa gtt 432
Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val
130 135 140
tcc gtg agt gaa cag gtg ttt ggc gaa ttg cct gaa gaa ttg gcg aaa 480
Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys
145 150 155 160
aaa cct aac ccg ttc gct gta tta gct aat tta aag aaa aac tag 525
Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn
165 170

<210> 159

<211> 174

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 159

Met Gln Lys Val Lys Leu Pro Leu Thr Ile Asp Pro Tyr Lys Asp Ala
1 5 10 15

Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn
20 25 30

Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr
35 40 45

Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr
50 55 60

Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe
65 70 75 80

Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met
85 90 95

Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn
100 105 110

Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile
115 120 125

Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val
130 135 140

Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys
145 150 155 160

Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn
165 170

<210> 160

<211> 1302

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> tig

<220>

<221> CDS

<222> (1)..(1299)

<400> 160

atg tca att tct att gaa act tta gaa ggc tta caa cgc cgc gta act 48
Met Ser Ile Ser Ile Glu Thr Leu Glu Gly Leu Gln Arg Arg Val Thr
1 5 10 15

att acc gta gct gct gat aaa atc gaa gcg gct tac aaa gag caa tta 96
Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu
20 25 30

aaa ggc tat gcg aaa aac gct cgt gta gac ggt ttc cgt aaa ggt aaa 144
Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys
35 40 45

gta ccg cac gca att atc gaa caa cgt ttc ggt tta gcg gct cgc caa	192
Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln	
50 55 60	
gac gta tta tcc gat gaa atg caa cgt gcg ttc ttt gat gcg gta atc	240
Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile	
65 70 75 80	
gct gag aaa att aac ctt gcc ggt cgt cct acc ttc aca ccg aac aac	288
Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn	
85 90 95	
tac caa ccg agt caa gaa ttc agc ttc act gca act ttt gaa gta ttc	336
Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe	
100 105 110	
ccg gaa gtt gaa tta aaa ggc tta gaa aat atc gaa gtt gaa aaa ccg	384
Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro	
115 120 125	
gtt gta gaa atc aca gaa gct gat tta gac aaa atg atc gat gtg tta	432
Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu	
130 135 140	
cgt aaa caa caa gcg act tgg gct gaa tct caa gca gcg gca caa gcg	480
Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala	
145 150 155 160	
gaa gac cgt gtt gta atc gac ttc gta ggt tct gta gac ggt gaa gag	528
Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu	
165 170 175	
ttt gaa ggc ggt aaa gcg aca gac ttc act tta gca atg ggt caa agt	576
Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser	
180 185 190	
cgt atg atc cct ggt ttt gaa gaa ggt atc gtt ggt cac aaa gcc ggc	624
Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly	
195 200 205	
gaa caa ttc gat atc gat gtt act ttc cct gaa gaa tac cac gct gaa	672
Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu	
210 215 220	
aac tta aaa ggt aaa gcg gcg aaa ttc gca att aca ctt aag aaa gta	720
Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val	
225 230 235 240	
gaa aat atc gta tta cct gaa tta acc gaa gaa ttc gtg aaa aaa ttc	768
Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe	
245 250 255	
ggt tca gca aaa act gta gaa gat tta cgt gcg gaa att aag aaa aat	816
Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn	
260 265 270	
atg caa cgt gaa ctt aaa aac gca gta acc gca cgc gtt aaa aac caa	864
Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln	
275 280 285	
gta atc aac ggt tta atc gca caa aat gaa att gaa gtg ccg gct gca	912
Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala	
290 295 300	

gct gta gct gaa gaa gtg gac gta tta cgt cgt caa gct gtt caa cgt	960
Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg	
305 310 315 320	
ttc ggt ggt aaa ccg gaa atg gct gca caa tta ccg gct gaa tta ttc	1008
Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe	
325 330 335	
gaa gct gat gca aaa cgt cgt gtt caa gta ggt tta tta ctt tca acc	1056
Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Ser Thr	
340 345 350	
gta atc ggt act aac gaa tta aaa gtt gat gaa aaa cgt gtt gaa gaa	1104
Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu	
355 360 365	
acg att gca gaa atc gct tca gct tac gaa caa ccg gct gaa gtt gtt	1152
Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val	
370 375 380	
gct cat tat gct gaa aaa aac cgt caa tta acc gaa aat atc cgt aac gta	1200
Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val	
385 390 395 400	
gtg tta gaa gag caa gct gtt gaa gtt gta ctt gct aaa gca aaa gta	1248
Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val	
405 410 415	
act gaa aaa gct act tct ttt gat gaa gta atg gct caa caa gct caa	1296
Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln	
420 425 430	
ggc taa	1302
Gly	

<210> 161
<211> 433
<212> PRT
<213> *Actinobacillus pleuropneumoniae*

<400> 161
Met Ser Ile Ser Ile Glu Thr Leu Glu Gly Leu Gln Arg Arg Val Thr
1 5 10 15

Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu
20 25 30

Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys
35 40 45

Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln
50 55 60

Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile
65 70 75 80

Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn
85 90 95

Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe
100 105 110

Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro
115 120 125

Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu
130 135 140

Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala
145 150 155 160

Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu
165 170 175

Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser
180 185 190

Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly
195 200 205

Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu
210 215 220

Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val
225 230 235 240

Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe
245 250 255

Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn
260 265 270

Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln
275 280 285

Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala
290 295 300

Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg
305 310 315 320

Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe
325 330 335

Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr
340 345 350

Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu
355 360 365

Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val
370 375 380

Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val
385 390 395 400

Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val
405 410 415

Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln
420 425 430

Gly

<210> 162
<211> 316
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> tRNA-glu

<400> 162
aatattgcgc tcaaatggca aaggcggagag catctttaaa tgggtcccc atcgtaga 60
ggccttaggac atcgcccttt cacggcgtt accgggggttc gaatccccgt ggggacgc 120
tttaaagatg acttttggc tctgaattgt tctttaaaaa attggaaaca agctgaaaac 180
tgagagatt tcgaaagaaa gtctgagtag taaaagataa gtaattatct tgaaaatctt 240
agctgaacaa aagcagctaa gtgttagtt gaataaaagta tcgcgttgaa tgcgttcaaa 300
taaaaatttga aaatat 316

<210> 163
<211> 85
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> tRNA-leu

<400> 163
gctctggtgg tggaaattggt agacacgcta tcttgagggg gtagtgtcca taggatgtgc 60
gagttcgagt ctcgcccaga gcacc 85

<210> 164
<211> 623
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> yaeE

<220>
<221> CDS
<222> (1)..(621)

<400> 164
atg caa gaa ctc aca cct caa atg tgg ggc tta gtc ggc act tca acg 48
Met Gln Glu Leu Thr Pro Gln Met Trp Gly Leu Val Gly Thr Ser Thr
1 5 10 15

ctt gaa acg ctc tat atg ggc ttt gcg gcg act tta ctt gct gtg gta 96
Leu Glu Thr Leu Tyr Met Gly Phe Ala Ala Thr Leu Leu Ala Val Val
20 25 30

gtc ggt ttg ccg atc ggt ttt ctg gca ttt tta acc ggt aaa gga gag 144
Val Gly Leu Pro Ile Gly Phe Leu Ala Phe Leu Thr Gly Lys Gly Glu
35 40 45

att tta gag aat ccg cgt tta cat caa gta tta gat gtg att att aat 192
Ile Leu Glu Asn Pro Arg Leu His Gln Val Leu Asp Val Ile Ile Asn

50	55	60	
atc ggt cgt tcc gta ccg ttt att att ttg tta gtc gtc ttg tta cct Ile Gly Arg Ser Val Pro Phe Ile Ile Leu Leu Val Val Leu Leu Pro 65 70 75 80			240
ttt acg cgt tta ttg gtc ggg aca acg ctc ggt act acg gcg gcg att Phe Thr Arg Leu Leu Val Gly Thr Thr Leu Gly Thr Thr Ala Ala Ile 85 90 95			288
gtg ccg tta agc gtt tcg gca att ccg ttt ttg gcg cgt tta act tca Val Pro Leu Ser Val Ser Ala Ile Pro Phe Phe Ala Arg Leu Thr Ser 100 105 110			336
aat gcg tta tta gaa atc cca gca ggt tta acc gaa gcg gcg aaa tcg Asn Ala Leu Leu Glu Ile Pro Ala Gly Leu Thr Glu Ala Ala Lys Ser 115 120 125			384
atg ggc gca acg aat tgg caa gtg gtc agt aaa ttg tat tta ccg gaa Met Gly Ala Thr Asn Trp Gln Val Val Ser Lys Phe Tyr Leu Pro Glu 130 135 140			432
tca ctg ccg att tta atc aat ggt atc aca tta act tta gtc gct tta Ser Leu Pro Ile Leu Ile Asn Gly Ile Thr Leu Thr Leu Val Ala Leu 145 150 155 160			480
atc ggt tat tcg gca atg gcg ggt gtc ggc ggc ggc ggt ttg ggt Ile Gly Tyr Ser Ala Met Ala Gly Ala Val Gly Gly Gly Leu Gly 165 170 175			528
aac ctt gcc atc agt tac ggt gaa cac cga aat atg gtc tat gta aaa Asn Leu Ala Ile Ser Tyr Gly Glu His Arg Asn Met Val Tyr Val Lys 180 185 190			576
tgg atc tca aca att att atc gta gcg att gtg atg atc agt caa aa Trp Ile Ser Thr Ile Ile Ile Val Ala Ile Val Met Ile Ser Gln 195 200 205			623
<210> 165			
<211> 207			
<212> PRT			
<213> <i>Actinobacillus pleuropneumoniae</i>			
<400> 165			
Met Gln Glu Leu Thr Pro Gln Met Trp Gly Leu Val Gly Thr Ser Thr 1 5 10 15			
Leu Glu Thr Leu Tyr Met Gly Phe Ala Ala Thr Leu Leu Ala Val Val 20 25 30			
Val Gly Leu Pro Ile Gly Phe Leu Ala Phe Leu Thr Gly Lys Gly Glu 35 40 45			
Ile Leu Glu Asn Pro Arg Leu His Gln Val Leu Asp Val Ile Ile Asn 50 55 60			
Ile Gly Arg Ser Val Pro Phe Ile Ile Leu Leu Val Val Leu Leu Pro 65 70 75 80			
Phe Thr Arg Leu Leu Val Gly Thr Thr Leu Gly Thr Thr Ala Ala Ile 85 90 95			

Val Pro Leu Ser Val Ser Ala Ile Pro Phe Phe Ala Arg Leu Thr Ser
100 105 110

Asn Ala Leu Leu Glu Ile Pro Ala Gly Leu Thr Glu Ala Ala Lys Ser
115 120 125

Met Gly Ala Thr Asn Trp Gln Val Val Ser Lys Phe Tyr Leu Pro Glu
130 135 140

Ser Leu Pro Ile Leu Ile Asn Gly Ile Thr Leu Thr Leu Val Ala Leu
145 150 155 160

Ile Gly Tyr Ser Ala Met Ala Gly Ala Val Gly Gly Gly Gly Leu Gly
165 170 175

Asn Leu Ala Ile Ser Tyr Gly Glu His Arg Asn Met Val Tyr Val Lys
180 185 190

Trp Ile Ser Thr Ile Ile Ile Val Ala Ile Val Met Ile Ser Gln
195 200 205